

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

- (i) APPLICANT: Guevera, Jr., Juan G.  
Hoogeveen, Ron C.  
Moore, Paul J.
- (ii) TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY  
VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
- (iii) NUMBER OF SEQUENCES: 229
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Arnold, White & Durkee
  - (B) STREET: P.O. Box 4433
  - (C) CITY: Houston
  - (D) STATE: Texas
  - (E) COUNTRY: USA
  - (F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US Unknown
  - (B) FILING DATE: Concurrently Herewith
  - (C) CLASSIFICATION: Unknown
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: McMillian, Nabeela R.
  - (B) REGISTRATION NUMBER: P-43,363
  - (C) REFERENCE/DOCKET NUMBER: ARAG:003
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 512/418-3000
  - (B) TELEFAX: 512/474-7577

### (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4536 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu	Glu	Glu	Met	Leu	Glu	Asn	Val	Ser	Leu	Val	Cys	Pro	Lys	Asp	Ala	
1				5					10					15		
Thr	Arg	Phe	Lys	His	Leu	Arg	Lys	Tyr	Thr	Tyr	Asn	Tyr	Glu	Ala	Glu	
			20					25					30			
Ser	Ser	Ser	Gly	Val	Pro	Gly	Thr	Ala	Asp	Ser	Arg	Ser	Ala	Thr	Arg	
			35				40					45				
Ile	Asn	Cys	Lys	Val	Glu	Leu	Glu	Val	Pro	Gln	Leu	Cys	Ser	Phe	Ile	
	50					55					60					
Leu	Lys	Thr	Ser	Gln	Cys	Thr	Leu	Lys	Glu	Val	Tyr	Gly	Phe	Asn	Pro	
65					70					75					80	
Glu	Gly	Lys	Ala	Leu	Leu	Lys	Lys	Thr	Lys	Asn	Ser	Glu	Glu	Phe	Ala	
				85					90					95		
Ala	Ala	Met	Ser	Arg	Tyr	Glu	Leu	Lys	Leu	Ala	Ile	Pro	Glu	Gly	Lys	
			100					105					110			
Gln	Val	Phe	Leu	Tyr	Pro	Glu	Lys	Asp	Glu	Pro	Thr	Tyr	Ile	Leu	Asn	
			115				120					125				
Ile	Lys	Arg	Gly	Ile	Ile	Ser	Ala	Leu	Leu	Val	Pro	Pro	Glu	Thr	Glu	
	130					135					140					
Glu	Ala	Lys	Gln	Val	Leu	Phe	Leu	Asp	Thr	Val	Tyr	Gly	Asn	Cys	Ser	
145					150					155					160	
Thr	His	Phe	Thr	Val	Lys	Thr	Arg	Lys	Gly	Asn	Val	Ala	Thr	Glu	Ile	
				165					170					175		
Ser	Thr	Glu	Arg	Asp	Leu	Gly	Gln	Cys	Asp	Arg	Phe	Lys	Pro	Ile	Arg	
				180				185					190			
Thr	Gly	Ile	Ser	Pro	Leu	Ala	Leu	Ile	Lys	Gly	Met	Thr	Arg	Pro	Leu	
		195					200					205				
Ser	Thr	Leu	Ile	Ser	Ser	Ser	Gln	Ser	Cys	Gln	Tyr	Thr	Leu	Asp	Ala	
	210					215					220					
Lys	Arg	Lys	His	Val	Ala	Glu	Ala	Ile	Cys	Lys	Glu	Gln	His	Leu	Phe	
225					230					235					240	
Leu	Pro	Phe	Ser	Tyr	Asn	Asn	Lys	Tyr	Gly	Met	Val	Ala	Gln	Val	Thr	
				245					250					255		
Gln	Thr	Leu	Lys	Leu	Glu	Asp	Thr	Pro	Lys	Ile	Asn	Ser	Arg	Phe	Phe	
				260				265					270			

Gly	Glu	Gly	Thr	Lys	Lys	Met	Gly	Leu	Ala	Phe	Glu	Ser	Thr	Lys	Ser		
		275					280					285					
Thr	Ser	Pro	Pro	Lys	Gln	Ala	Glu	Ala	Val	Leu	Lys	Thr	Leu	Gln	Glu		
	290					295					300						
Leu	Lys	Lys	Leu	Thr	Ile	Ser	Glu	Gln	Asn	Ile	Gln	Arg	Ala	Asn	Leu		
305					310					315					320		
Phe	Asn	Lys	Leu	Val	Thr	Glu	Leu	Arg	Gly	Leu	Ser	Asp	Glu	Ala	Val		
				325					330					335			
Thr	Ser	Leu	Leu	Pro	Gln	Leu	Ile	Glu	Val	Ser	Ser	Pro	Ile	Thr	Leu		
			340					345					350				
Gln	Ala	Leu	Val	Gln	Cys	Gly	Gln	Pro	Gln	Cys	Ser	Thr	His	Ile	Leu		
	355						360					365					
Gln	Trp	Leu	Lys	Arg	Val	His	Ala	Asn	Pro	Leu	Leu	Ile	Asp	Val	Val		
	370					375					380						
Thr	Tyr	Leu	Val	Ala	Leu	Ile	Pro	Glu	Pro	Ser	Ala	Gln	Gln	Leu	Arg		
385					390					395					400		
Glu	Ile	Phe	Asn	Met	Ala	Arg	Asp	Gln	Arg	Ser	Arg	Ala	Thr	Leu	Tyr		
				405					410					415			
Ala	Leu	Ser	His	Ala	Val	Asn	Asn	Tyr	His	Lys	Thr	Asn	Pro	Thr	Gly		
			420					425					430				
Thr	Gln	Glu	Leu	Leu	Asp	Ile	Ala	Asn	Tyr	Leu	Met	Glu	Gln	Ile	Gln		
		435					440					445					
Asp	Asp	Cys	Thr	Gly	Asp	Glu	Asp	Tyr	Thr	Tyr	Leu	Ile	Leu	Arg	Val		
	450					455					460						
Ile	Gly	Asn	Met	Gly	Gln	Thr	Met	Glu	Gln	Leu	Thr	Pro	Glu	Leu	Lys		
465					470					475					480		
Ser	Ser	Ile	Leu	Lys	Cys	Val	Gln	Ser	Thr	Lys	Pro	Ser	Leu	Met	Ile		
				485					490					495			
Gln	Lys	Ala	Ala	Ile	Gln	Ala	Leu	Arg	Lys	Met	Glu	Pro	Lys	Asp	Lys		
			500					505					510				
Asp	Gln	Glu	Val	Leu	Leu	Gln	Thr	Phe	Leu	Asp	Asp	Ala	Ser	Pro	Gly		
		515					520					525					
Asp	Lys	Arg	Leu	Ala	Ala	Tyr	Leu	Met	Leu	Met	Arg	Ser	Pro	Ser	Gln		
	530					535					540						
Ala	Asp	Ile	Asn	Lys	Ile	Val	Gln	Ile	Leu	Pro	Trp	Glu	Gln	Asn	Glu		
545					550					555					560		

Gln Val Lys Asn Phe Val Ala Ser His Ile Ala Asn Ile Leu Asn Ser  
 565 570 575  
 Glu Glu Leu Asp Ile Gln Asp Leu Lys Lys Leu Val Lys Glu Ala Leu  
 580 585 590  
 Lys Glu Ser Gln Leu Pro Thr Val Met Asp Phe Arg Lys Phe Ser Arg  
 595 600 605  
 Asn Tyr Gln Leu Tyr Lys Ser Val Ser Leu Pro Ser Leu Asp Pro Ala  
 610 615 620  
 Ser Ala Lys Ile Glu Gly Asn Leu Ile Phe Asp Pro Asn Asn Tyr Leu  
 625 630 635 640  
 Pro Lys Glu Ser Met Leu Lys Thr Thr Leu Thr Ala Phe Gly Phe Ala  
 645 650 655  
 Ser Ala Asp Leu Ile Glu Ile Gly Leu Glu Gly Lys Gly Phe Glu Pro  
 660 665 670  
 Thr Leu Glu Ala Leu Phe Gly Lys Gln Gly Phe Phe Pro Asp Ser Val  
 675 680 685  
 Asn Lys Ala Leu Tyr Trp Val Asn Gly Gln Val Pro Asp Gly Val Ser  
 690 695 700  
 Lys Val Leu Val Asp His Phe Gly Tyr Thr Lys Asp Asp Lys His Glu  
 705 710 715 720  
 Gln Asp Met Val Asn Gly Ile Met Leu Ser Val Glu Lys Leu Ile Lys  
 725 730 735  
 Asp Leu Lys Ser Lys Glu Val Pro Glu Ala Arg Ala Tyr Leu Arg Ile  
 740 745 750  
 Leu Gly Glu Glu Leu Gly Phe Ala Ser Leu His Asp Leu Gln Leu Leu  
 755 760 765  
 Gly Lys Leu Leu Leu Met Gly Ala Arg Thr Leu Gln Gly Ile Pro Gln  
 770 775 780  
 Met Ile Gly Glu Val Ile Arg Lys Gly Ser Lys Asn Asp Phe Phe Leu  
 785 790 795 800  
 His Tyr Ile Phe Met Glu Asn Ala Phe Glu Leu Pro Thr Gly Ala Gly  
 805 810 815  
 Leu Gln Leu Gln Ile Ser Ser Ser Gly Val Ile Ala Pro Gly Ala Lys  
 820 825 830  
 Ala Gly Val Lys Leu Glu Val Ala Asn Met Gln Ala Glu Leu Val Ala  
 835 840 845



Lys Pro Ser Val Ser Val Glu Phe Val Thr Asn Met Gly Ile Ile Ile  
 850 855 860

Pro Asp Phe Ala Arg Ser Gly Val Gln Met Asn Thr Asn Phe Phe His  
 865 870 875 880

Glu Ser Gly Leu Glu Ala His Val Ala Leu Lys Ala Gly Lys Leu Lys  
 885 890 895

Phe Ile Ile Pro Ser Pro Lys Arg Pro Val Lys Leu Leu Ser Gly Gly  
 900 905 910

Asn Thr Leu His Leu Val Ser Thr Thr Lys Thr Glu Val Ile Pro Pro  
 915 920 925

Leu Ile Glu Asn Arg Gln Ser Trp Ser Val Cys Lys Gln Val Phe Pro  
 930 935 940

Gly Leu Asn Tyr Cys Thr Ser Gly Ala Tyr Ser Asn Ala Ser Ser Thr  
 945 950 955 960

Asp Ser Ala Ser Tyr Tyr Pro Leu Thr Gly Asp Thr Arg Leu Glu Leu  
 965 970 975

Glu Leu Arg Pro Thr Gly Glu Ile Glu Gln Tyr Ser Val Ser Ala Thr  
 980 985 990

Tyr Glu Leu Gln Arg Glu Asp Arg Ala Leu Val Asp Thr Leu Lys Phe  
 995 1000 1005

Val Thr Gln Ala Glu Gly Ala Lys Gln Thr Glu Ala Thr Met Thr Phe  
 1010 1015 1020

Lys Tyr Asn Arg Gln Ser Met Thr Leu Ser Ser Glu Val Gln Ile Pro  
 1025 1030 1035 1040

Asp Phe Asp Val Asp Leu Gly Thr Ile Leu Arg Val Asn Asp Glu Ser  
 1045 1050 1055

Thr Glu Gly Lys Thr Ser Tyr Arg Leu Thr Leu Asp Ile Gln Asn Lys  
 1060 1065 1070

Lys Ile Thr Glu Val Ala Leu Met Gly His Leu Ser Cys Asp Thr Lys  
 1075 1080 1085

Glu Glu Arg Lys Ile Lys Gly Val Ile Ser Ile Pro Arg Leu Gln Ala  
 1090 1095 1100

Glu Ala Arg Ser Glu Ile Leu Ala His Trp Ser Pro Ala Lys Leu Leu  
 1105 1110 1115 1120

Leu Gln Met Asp Ser Ser Ala Thr Ala Tyr Gly Ser Thr Val Ser Lys  
 1125 1130 1135

Arg Val Ala Trp His Tyr Asp Glu Glu Lys Ile Glu Phe Glu Trp Asn  
 1140 1145 1150  
 Thr Gly Thr Asn Val Asp Thr Lys Lys Met Thr Ser Asn Phe Pro Val  
 1155 1160 1165  
 Asp Leu Ser Asp Tyr Pro Lys Ser Leu His Met Tyr Ala Asn Arg Leu  
 1170 1175 1180  
 Leu Asp His Arg Val Pro Glu Thr Asp Met Thr Phe Arg His Val Gly  
 1185 1190 1195 1200  
 Ser Lys Leu Ile Val Ala Met Ser Ser Trp Leu Gln Lys Ala Ser Gly  
 1205 1210 1215  
 Ser Leu Pro Tyr Thr Gln Thr Leu Gln Asp His Leu Asn Ser Leu Lys  
 1220 1225 1230  
 Glu Phe Asn Leu Gln Asn Met Gly Leu Pro Asp Phe His Ile Pro Glu  
 1235 1240 1245  
 Asn Leu Phe Leu Lys Ser Asp Gly Arg Val Lys Tyr Thr Leu Asn Lys  
 1250 1255 1260  
 Asn Ser Leu Lys Ile Glu Ile Pro Leu Pro Phe Gly Gly Lys Ser Ser  
 1265 1270 1275 1280  
 Arg Asp Leu Lys Met Leu Glu Thr Val Arg Thr Pro Ala Leu His Phe  
 1285 1290 1295  
 Lys Ser Val Gly Phe His Leu Pro Ser Arg Glu Phe Gln Val Pro Thr  
 1300 1305 1310  
 Phe Thr Ile Pro Lys Leu Tyr Gln Leu Gln Val Pro Leu Leu Gly Val  
 1315 1320 1325  
 Leu Asp Leu Ser Thr Asn Val Tyr Ser Asn Leu Tyr Asn Trp Ser Ala  
 1330 1335 1340  
 Ser Tyr Ser Gly Gly Asn Thr Ser Thr Asp His Phe Ser Leu Arg Ala  
 1345 1350 1355 1360  
 Arg Tyr His Met Lys Ala Asp Ser Val Val Asp Leu Leu Ser Tyr Asn  
 1365 1370 1375  
 Val Gln Gly Ser Gly Glu Thr Thr Tyr Asp His Lys Asn Thr Phe Thr  
 1380 1385 1390  
 Leu Ser Cys Asp Gly Ser Leu Arg His Lys Phe Leu Asp Ser Asn Ile  
 1395 1400 1405  
 Lys Phe Ser His Val Glu Lys Leu Gly Asn Asn Pro Val Ser Lys Gly  
 1410 1415 1420

Leu Leu Ile Phe Asp Ala Ser Ser Ser Trp Gly Pro Gln Met Ser Ala  
 1425 1430 1435 1440

Ser Val His Leu Asp Ser Lys Lys Lys Gln His Leu Phe Val Lys Glu  
 1445 1450 1455

Val Lys Ile Asp Gly Gln Phe Arg Val Ser Ser Phe Tyr Ala Lys Gly  
 1460 1465 1470

Thr Tyr Gly Leu Ser Cys Gln Arg Asp Pro Asn Thr Gly Arg Leu Asn  
 1475 1480 1485

Gly Glu Ser Asn Leu Arg Phe Asn Ser Ser Tyr Leu Gln Gly Thr Asn  
 1490 1495 1500

Gln Ile Thr Gly Arg Tyr Glu Asp Gly Thr Leu Ser Leu Thr Ser Thr  
 1505 1510 1515 1520

Ser Asp Leu Gln Ser Gly Ile Ile Lys Asn Thr Ala Ser Leu Lys Tyr  
 1525 1530 1535

Glu Asn Tyr Glu Leu Thr Leu Lys Ser Asp Thr Asn Gly Lys Tyr Lys  
 1540 1545 1550

Asn Phe Ala Thr Ser Asn Lys Met Asp Met Thr Phe Ser Lys Gln Asn  
 1555 1560 1565

Ala Leu Leu Arg Ser Glu Tyr Gln Ala Asp Tyr Glu Ser Leu Arg Phe  
 1570 1575 1580

Phe Ser Leu Leu Ser Gly Ser Leu Asn Ser His Gly Leu Glu Leu Asn  
 1585 1590 1595 1600

Ala Asp Ile Leu Gly Thr Asp Lys Ile Asn Ser Gly Ala His Lys Ala  
 1605 1610 1615

Thr Leu Arg Ile Gly Gln Asp Gly Ile Ser Thr Ser Ala Thr Thr Asn  
 1620 1625 1630

Leu Lys Cys Ser Leu Leu Val Leu Glu Asn Glu Leu Asn Ala Glu Leu  
 1635 1640 1645

Gly Leu Ser Gly Ala Ser Met Lys Leu Thr Thr Asn Gly Arg Phe Arg  
 1650 1655 1660

Glu His Asn Ala Lys Phe Ser Leu Asp Gly Lys Ala Ala Leu Thr Glu  
 1665 1670 1675 1680

Leu Ser Leu Gly Ser Ala Tyr Gln Ala Met Ile Leu Gly Val Asp Ser  
 1685 1690 1695

Lys Asn Ile Phe Asn Phe Lys Val Ser Gln Glu Gly Leu Lys Leu Ser  
 1700 1705 1710

Asn Asp Met Met Gly Ser Tyr Ala Glu Met Lys Phe Asp His Thr Asn  
 1715 1720 1725  
 Ser Leu Asn Ile Ala Gly Leu Ser Leu Asp Phe Ser Ser Lys Leu Asp  
 1730 1735 1740  
 Asn Ile Tyr Ser Ser Asp Lys Phe Tyr Lys Gln Thr Val Asn Leu Gln  
 1745 1750 1755 1760  
 Leu Gln Pro Tyr Ser Leu Val Thr Thr Leu Asn Ser Asp Leu Lys Tyr  
 1765 1770 1775  
 Asn Ala Leu Asp Leu Thr Asn Asn Gly Lys Leu Arg Leu Glu Pro Leu  
 1780 1785 1790  
 Lys Leu His Val Ala Gly Asn Leu Lys Gly Ala Tyr Gln Asn Asn Glu  
 1795 1800 1805  
 Ile Lys His Ile Tyr Ala Ile Ser Ser Ala Ala Leu Ser Ala Ser Tyr  
 1810 1815 1820  
 Lys Ala Asp Thr Val Ala Lys Val Gln Gly Val Glu Phe Ser His Arg  
 1825 1830 1835 1840  
 Leu Asn Thr Asp Ile Ala Gly Leu Ala Ser Ala Ile Asp Met Ser Thr  
 1845 1850 1855  
 Asn Tyr Asn Ser Asp Ser Leu His Phe Ser Asn Val Phe Arg Ser Val  
 1860 1865 1870  
 Met Ala Pro Phe Thr Met Thr Ile Asp Ala His Thr Asn Gly Asn Gly  
 1875 1880 1885  
 Lys Leu Ala Leu Trp Gly Glu His Thr Gly Gln Leu Tyr Ser Lys Phe  
 1890 1895 1900  
 Leu Leu Lys Ala Glu Pro Leu Ala Phe Thr Phe Ser His Asp Tyr Lys  
 1905 1910 1915 1920  
 Gly Ser Thr Ser His His Leu Val Ser Arg Lys Ser Ile Ser Ala Ala  
 1925 1930 1935  
 Leu Glu His Lys Val Ser Ala Leu Leu Thr Pro Ala Glu Gln Thr Gly  
 1940 1945 1950  
 Thr Trp Lys Leu Lys Thr Gln Phe Asn Asn Asn Glu Tyr Ser Gln Asp  
 1955 1960 1965  
 Leu Asp Ala Tyr Asn Thr Lys Asp Lys Ile Gly Val Glu Leu Thr Gly  
 1970 1975 1980  
 Arg Thr Leu Ala Asp Leu Thr Leu Leu Asp Ser Pro Ile Lys Val Pro  
 1985 1990 1995 2000

Leu Leu Leu Ser Glu Pro Ile Asn Ile Ile Asp Ala Leu Glu Met Arg  
 2005 2010 2015  
 Asp Ala Val Glu Lys Pro Gln Glu Phe Thr Ile Val Ala Phe Val Lys  
 2020 2025 2030  
 Tyr Asp Lys Asn Gln Asp Val His Ser Ile Asn Leu Pro Phe Phe Glu  
 2035 2040 2045  
 Thr Leu Gln Glu Tyr Phe Glu Arg Asn Arg Gln Thr Ile Ile Val Val  
 2050 2055 2060  
 Val Glu Asn Val Gln Arg Asn Leu Lys His Ile Asn Ile Asp Gln Phe  
 2065 2070 2075 2080  
 Val Arg Lys Tyr Arg Ala Ala Leu Gly Lys Leu Pro Gln Gln Ala Asn  
 2085 2090 2095  
 Asp Tyr Leu Asn Ser Phe Asn Trp Glu Arg Gln Val Ser His Ala Lys  
 2100 2105 2110  
 Glu Lys Leu Thr Ala Leu Thr Lys Lys Tyr Arg Ile Thr Glu Asn Asp  
 2115 2120 2125  
 Ile Gln Ile Ala Leu Asp Asp Ala Lys Ile Asn Phe Asn Glu Lys Leu  
 2130 2135 2140  
 Ser Gln Leu Gln Thr Tyr Met Ile Gln Phe Asp Gln Tyr Ile Lys Asp  
 2145 2150 2155 2160  
 Ser Tyr Asp Leu His Asp Leu Lys Ile Ala Ile Ala Asn Ile Ile Asp  
 2165 2170 2175  
 Glu Ile Ile Glu Lys Leu Lys Ser Leu Asp Glu His Tyr His Ile Arg  
 2180 2185 2190  
 Val Asn Leu Val Lys Thr Ile His Asp Leu His Leu Phe Ile Glu Asn  
 2195 2200 2205  
 Ile Asp Phe Asn Lys Ser Gly Ser Ser Thr Ala Ser Trp Ile Gln Asn  
 2210 2215 2220  
 Val Asp Thr Lys Tyr Gln Ile Arg Ile Gln Ile Gln Glu Lys Leu Gln  
 2225 2230 2235 2240  
 Gln Leu Lys Arg His Ile Gln Asn Ile Asp Ile Gln His Leu Ala Gly  
 2245 2250 2255  
 Lys Leu Lys Gln His Ile Glu Ala Ile Asp Val Arg Val Leu Leu Asp  
 2260 2265 2270  
 Gln Leu Gly Thr Thr Ile Ser Phe Glu Arg Ile Asn Asp Val Leu Glu  
 2275 2280 2285

His Val Lys His Phe Val Ile Asn Leu Ile Gly Asp Phe Glu Val Ala  
 2290 2295 2300

Glu Lys Ile Asn Ala Phe Arg Ala Lys Val His Glu Leu Ile Glu Arg  
 2305 2310 2315 2320

Tyr Glu Val Asp Gln Gln Ile Gln Val Leu Met Asp Lys Leu Val Glu  
 2325 2330 2335

Leu Thr His Gln Tyr Lys Leu Lys Glu Thr Ile Gln Lys Leu Ser Asn  
 2340 2345 2350

Val Leu Gln Gln Val Lys Ile Lys Asp Tyr Phe Glu Lys Leu Val Gly  
 2355 2360 2365

Phe Ile Asp Asp Ala Val Lys Lys Leu Asn Glu Leu Ser Phe Lys Thr  
 2370 2375 2380

Phe Ile Glu Asp Val Asn Lys Phe Leu Asp Met Leu Ile Lys Lys Leu  
 2385 2390 2395 2400

Lys Ser Phe Asp Tyr His Gln Phe Val Asp Glu Thr Asn Asp Lys Ile  
 2405 2410 2415

Arg Glu Val Thr Gln Arg Leu Asn Gly Glu Ile Gln Ala Leu Glu Leu  
 2420 2425 2430

Pro Gln Lys Ala Glu Ala Leu Lys Leu Phe Leu Glu Glu Thr Lys Ala  
 2435 2440 2445

Thr Val Ala Val Tyr Leu Glu Ser Leu Gln Asp Thr Lys Ile Thr Leu  
 2450 2455 2460

Ile Ile Asn Trp Leu Gln Glu Ala Leu Ser Ser Ala Ser Leu Ala His  
 2465 2470 2475 2480

Met Lys Ala Lys Phe Arg Glu Thr Leu Glu Asp Thr Arg Asp Arg Met  
 2485 2490 2495

Tyr Asp Met Asp Ile Gln Gln Glu Leu Gln Arg Tyr Leu Ser Leu Val  
 2500 2505 2510

Gly Gln Val Tyr Ser Thr Leu Val Thr Tyr Ile Ser Asp Trp Trp Thr  
 2515 2520 2525

Leu Ala Ala Lys Asn Leu Thr Asp Phe Ala Glu Gln Tyr Ser Ile Gln  
 2530 2535 2540

Asp Trp Ala Lys Arg Met Lys Ala Leu Val Glu Gln Gly Phe Thr Val  
 2545 2550 2555 2560

Pro Glu Ile Lys Thr Ile Leu Gly Thr Met Pro Ala Phe Glu Val Ser  
 2565 2570 2575

Leu Gln Ala	Leu Gln Lys	Ala Thr	Phe Gln Thr	Pro Asp	Phe Ile Val
2580			2585		2590
Pro Leu Thr	Asp Leu Arg	Ile Pro	Ser Val Gln	Ile Asn	Phe Lys Asp
2595		2600		2605	
Leu Lys Asn	Ile Lys Ile	Pro Ser	Arg Phe Ser	Thr Pro	Glu Phe Thr
2610		2615		2620	
Ile Leu Asn	Thr Phe His	Ile Pro	Ser Phe Thr	Ile Asp	Phe Val Glu
2625		2630		2635	2640
Met Lys Val	Lys Ile Ile	Arg Thr	Ile Asp	Gln Met	Gln Asn Ser Glu
	2645		2650		2655
Leu Gln Trp	Pro Val Pro	Asp Ile	Tyr Leu Arg	Asp Leu	Lys Val Glu
	2660		2665		2670
Asp Ile Pro	Leu Ala Arg	Ile Thr	Leu Pro Asp	Phe Arg	Leu Pro Glu
	2675		2680		2685
Ile Ala Ile	Pro Glu Phe	Ile Ile	Pro Thr	Leu Asn	Leu Asn Asp Phe
2690		2695		2700	
Gln Val Pro	Asp Leu His	Ile Pro	Glu Phe Gln	Leu Pro	His Ile Ser
2705		2710		2715	2720
His Thr Ile	Glu Val Pro	Thr Phe	Gly Lys Leu	Tyr Ser	Ile Leu Lys
	2725		2730		2735
Ile Gln Ser	Pro Leu Phe	Thr Leu	Asp Ala Asn	Ala Asp	Ile Gly Asn
	2740		2745		2750
Gly Thr Thr	Ser Ala Asn	Glu Ala	Gly Ile Ala	Ala Ser	Ile Thr Ala
	2755		2760		2765
Lys Gly Glu	Ser Lys Leu	Glu Val	Leu Asn Phe	Asp Phe	Gln Ala Asn
2770		2775		2780	
Ala Gln Leu	Ser Asn Pro	Lys Ile	Asn Pro Leu	Ala Leu	Lys Glu Ser
2785		2790		2795	2800
Val Lys Phe	Ser Ser Lys	Tyr Leu	Arg Thr	Glu His	Gly Ser Glu Met
	2805		2810		2815
Leu Phe Phe	Gly Asn Ala	Ile Glu	Gly Lys Ser	Asn Thr	Val Ala Ser
	2820		2825		2830
Leu His Thr	Glu Lys Asn	Thr Leu	Glu Leu Ser	Asn Gly	Val Ile Val
	2835		2840		2845
Lys Ile Asn	Asn Gln Leu	Thr Leu	Asp Ser Asn	Thr Lys	Tyr Phe His
2850		2855		2860	

Lys Leu Asn Ile Pro Lys Leu Asp Phe Ser Ser Gln Ala Asp Leu Arg			
2865	2870	2875	2880
Asn Glu Ile Lys Thr Leu Leu Lys Ala Gly His Ile Ala Trp Thr Ser			
	2885	2890	2895
Ser Gly Lys Gly Ser Trp Lys Trp Ala Cys Pro Arg Phe Ser Asp Glu			
	2900	2905	2910
Gly Thr His Glu Ser Gln Ile Ser Phe Thr Ile Glu Gly Pro Leu Thr			
	2915	2920	2925
Ser Phe Gly Leu Ser Asn Lys Ile Asn Ser Lys His Leu Arg Val Asn			
	2930	2935	2940
Gln Asn Leu Val Tyr Glu Ser Gly Ser Leu Asn Phe Ser Lys Leu Glu			
2945	2950	2955	2960
Ile Gln Ser Gln Val Asp Ser Gln His Val Gly His Ser Val Leu Thr			
	2965	2970	2975
Ala Lys Gly Met Ala Leu Phe Gly Glu Gly Lys Ala Glu Phe Thr Gly			
	2980	2985	2990
Arg His Asp Ala His Leu Asn Gly Lys Val Ile Gly Thr Leu Lys Asn			
	2995	3000	3005
Ser Leu Phe Phe Ser Ala Gln Pro Phe Glu Ile Thr Ala Ser Thr Asn			
	3010	3015	3020
Asn Glu Gly Asn Leu Lys Val Arg Phe Pro Leu Arg Leu Thr Gly Lys			
3025	3030	3035	3040
Ile Asp Phe Leu Asn Asn Tyr Ala Leu Phe Leu Ser Pro Ser Ala Gln			
	3045	3050	3055
Gln Ala Ser Trp Gln Val Ser Ala Arg Phe Asn Gln Tyr Lys Tyr Asn			
	3060	3065	3070
Gln Asn Phe Ser Ala Gly Asn Asn Glu Asn Ile Met Glu Ala His Val			
	3075	3080	3085
Gly Ile Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn Ile Pro Leu Thr			
	3090	3095	3100
Ile Pro Glu Met Arg Leu Pro Tyr Thr Ile Ile Thr Thr Pro Pro Leu			
3105	3110	3115	3120
Lys Asp Phe Ser Leu Trp Glu Lys Thr Gly Leu Lys Glu Phe Leu Lys			
	3125	3130	3135
Thr Thr Lys Gln Ser Phe Asp Leu Ser Val Lys Ala Gln Tyr Lys Lys			
	3140	3145	3150



Asn Lys His Arg His Ser Ile Thr Asn Pro Leu Ala Val Leu Cys Glu  
 3155 3160 3165  
 Phe Ile Ser Gln Ser Ile Lys Ser Phe Asp Arg His Phe Glu Lys Asn  
 3170 3175 3180  
 Arg Asn Asn Ala Leu Asp Phe Val Thr Lys Ser Tyr Asn Glu Thr Lys  
 3185 3190 3195 3200  
 Ile Lys Phe Asp Lys Tyr Lys Ala Glu Lys Ser His Asp Glu Leu Pro  
 3205 3210 3215  
 Arg Thr Phe Gln Ile Pro Gly Tyr Thr Val Pro Val Val Asn Val Glu  
 3220 3225 3230  
 Val Ser Pro Phe Thr Ile Glu Met Ser Ala Phe Gly Tyr Val Phe Pro  
 3235 3240 3245  
 Lys Ala Val Ser Met Pro Ser Phe Ser Ile Leu Gly Ser Asp Val Arg  
 3250 3255 3260  
 Val Pro Ser Tyr Thr Leu Ile Leu Pro Ser Leu Glu Leu Pro Val Leu  
 3265 3270 3275 3280  
 His Val Pro Arg Asn Leu Lys Leu Ser Leu Pro His Phe Lys Glu Leu  
 3285 3290 3295  
 Cys Thr Ile Ser His Ile Phe Ile Pro Ala Met Gly Asn Ile Thr Tyr  
 3300 3305 3310  
 Asp Phe Ser Phe Lys Ser Ser Val Ile Thr Leu Asn Thr Asn Ala Glu  
 3315 3320 3325  
 Leu Phe Asn Gln Ser Asp Ile Val Ala His Leu Leu Ser Ser Ser Ser  
 3330 3335 3340  
 Ser Val Ile Asp Ala Leu Gln Tyr Lys Leu Glu Gly Thr Thr Arg Leu  
 3345 3350 3355 3360  
 Thr Arg Lys Arg Gly Leu Lys Leu Ala Thr Ala Leu Ser Leu Ser Asn  
 3365 3370 3375  
 Lys Phe Val Glu Gly Ser His Asn Ser Thr Val Ser Leu Thr Thr Lys  
 3380 3385 3390  
 Asn Met Glu Val Ser Val Ala Lys Thr Thr Lys Ala Glu Ile Pro Ile  
 3395 3400 3405  
 Leu Arg Met Asn Phe Lys Gln Glu Leu Asn Gly Asn Thr Lys Ser Lys  
 3410 3415 3420  
 Pro Thr Val Ser Ser Ser Met Glu Phe Lys Tyr Asp Phe Asn Ser Ser  
 3425 3430 3435 3440

Met Leu Tyr Ser Thr Ala Lys Gly Ala Val Asp His Lys Leu Ser Leu  
 3445 3450 3455  
 Glu Ser Leu Thr Ser Tyr Phe Ser Ile Glu Ser Ser Thr Lys Gly Asp  
 3460 3465 3470  
 Val Lys Gly Ser Val Leu Ser Arg Glu Tyr Ser Gly Thr Ile Ala Ser  
 3475 3480 3485  
 Glu Ala Asn Thr Tyr Leu Asn Ser Lys Ser Thr Arg Ser Ser Val Lys  
 3490 3495 3500  
 Leu Gln Gly Thr Ser Lys Ile Asp Asp Ile Trp Asn Leu Glu Val Lys  
 3505 3510 3515 3520  
 Glu Asn Phe Ala Gly Glu Ala Thr Leu Gln Arg Ile Tyr Ser Leu Trp  
 3525 3530 3535  
 Glu His Ser Thr Lys Asn His Leu Gln Leu Glu Gly Leu Phe Phe Thr  
 3540 3545 3550  
 Asn Gly Glu His Thr Ser Lys Ala Thr Leu Glu Leu Ser Pro Trp Gln  
 3555 3560 3565  
 Met Ser Ala Leu Val Gln Val His Ala Ser Gln Pro Ser Ser Phe His  
 3570 3575 3580  
 Asp Phe Pro Asp Leu Gly Gln Glu Val Ala Leu Asn Ala Asn Thr Lys  
 3585 3590 3595 3600  
 Asn Gln Lys Ile Arg Trp Lys Asn Glu Val Arg Ile His Ser Gly Ser  
 3605 3610 3615  
 Phe Gln Ser Gln Val Glu Leu Ser Asn Asp Gln Glu Lys Ala His Leu  
 3620 3625 3630  
 Asp Ile Ala Gly Ser Leu Glu Gly His Leu Arg Phe Leu Lys Asn Ile  
 3635 3640 3645  
 Ile Leu Pro Val Tyr Asp Lys Ser Leu Trp Asp Phe Leu Lys Leu Asp  
 3650 3655 3660  
 Val Thr Thr Ser Ile Gly Arg Arg Gln His Leu Arg Val Ser Thr Ala  
 3665 3670 3675 3680  
 Phe Val Tyr Thr Lys Asn Pro Asn Gly Tyr Ser Phe Ser Ile Pro Val  
 3685 3690 3695  
 Lys Val Leu Ala Asp Lys Phe Ile Thr Pro Gly Leu Lys Leu Asn Asp  
 3700 3705 3710  
 Leu Asn Ser Val Leu Val Met Pro Thr Phe His Val Pro Phe Thr Asp  
 3715 3720 3725

Leu Gln Val Pro Ser Cys Lys Leu Asp Phe Arg Glu Ile Gln Ile Tyr  
 3730 3735 3740

Lys Lys Leu Arg Thr Ser Ser Phe Ala Leu Asn Leu Pro Thr Leu Pro  
 3745 3750 3755 3760

Glu Val Lys Phe Pro Glu Val Asp Val Leu Thr Lys Tyr Ser Gln Pro  
 3765 3770 3775

Glu Asp Ser Leu Ile Pro Phe Phe Glu Ile Thr Val Pro Glu Ser Gln  
 3780 3785 3790

Leu Thr Val Ser Gln Phe Thr Leu Pro Lys Ser Val Ser Asp Gly Ile  
 3795 3800 3805

Ala Ala Leu Asp Leu Asn Ala Val Ala Asn Lys Ile Ala Asp Phe Glu  
 3810 3815 3820

Leu Pro Thr Ile Ile Val Pro Glu Gln Thr Ile Glu Ile Pro Ser Ile  
 3825 3830 3835 3840

Lys Phe Ser Val Pro Ala Gly Ile Val Ile Pro Ser Phe Gln Ala Leu  
 3845 3850 3855

Thr Ala Arg Phe Glu Val Asp Ser Pro Val Tyr Asn Ala Thr Trp Ser  
 3860 3865 3870

Ala Ser Leu Lys Asn Lys Ala Asp Tyr Val Glu Thr Val Leu Asp Ser  
 3875 3880 3885

Thr Cys Ser Ser Thr Val Gln Phe Leu Glu Tyr Glu Leu Asn Val Leu  
 3890 3895 3900

Gly Thr His Lys Ile Glu Asp Gly Thr Leu Ala Ser Lys Thr Lys Gly  
 3905 3910 3915 3920

Thr Leu Ala His Arg Asp Phe Ser Ala Glu Tyr Glu Glu Asp Gly Lys  
 3925 3930 3935

Phe Glu Gly Leu Gln Glu Trp Glu Gly Lys Ala His Leu Asn Ile Lys  
 3940 3945 3950

Ser Pro Ala Phe Thr Asp Leu His Leu Arg Tyr Gln Lys Asp Lys Lys  
 3955 3960 3965

Gly Ile Ser Thr Ser Ala Ala Ser Pro Ala Val Gly Thr Val Gly Met  
 3970 3975 3980

Asp Met Asp Glu Asp Asp Asp Phe Ser Lys Trp Asn Phe Tyr Tyr Ser  
 3985 3990 3995 4000

Pro Gln Ser Ser Pro Asp Lys Lys Leu Thr Ile Phe Lys Thr Glu Leu  
 4005 4010 4015

Arg Val Arg Glu Ser Asp Glu Glu Thr Gln Ile Lys Val Asn Trp Glu		
4020	4025	4030
Glu Glu Ala Ala Ser Gly Leu Leu Thr Ser Leu Lys Asp Asn Val Pro		
4035	4040	4045
Lys Ala Thr Gly Val Leu Tyr Asp Tyr Val Asn Lys Tyr His Trp Glu		
4050	4055	4060
His Thr Gly Leu Thr Leu Arg Glu Val Ser Ser Lys Leu Arg Arg Asn		
4065	4070	4075 4080
Leu Gln Asn Asn Ala Glu Trp Val Tyr Gln Gly Ala Ile Arg Gln Ile		
4085	4090	4095
Asp Asp Ile Asp Val Arg Phe Gln Lys Ala Ala Ser Gly Thr Thr Gly		
4100	4105	4110
Thr Tyr Gln Glu Trp Lys Asp Lys Ala Gln Asn Leu Tyr Gln Glu Leu		
4115	4120	4125
Leu Thr Gln Glu Gly Gln Ala Ser Phe Gln Gly Leu Lys Asp Asn Val		
4130	4135	4140
Phe Asp Gly Leu Val Arg Val Thr Gln Lys Phe His Met Lys Val Lys		
4145	4150	4155 4160
His Leu Ile Asp Ser Leu Ile Asp Phe Leu Asn Phe Pro Arg Phe Gln		
4165	4170	4175
Phe Pro Gly Lys Pro Gly Ile Tyr Thr Arg Glu Glu Leu Cys Thr Met		
4180	4185	4190
Phe Ile Arg Glu Val Gly Thr Val Leu Ser Gln Val Tyr Ser Lys Val		
4195	4200	4205
His Asn Gly Ser Glu Ile Leu Phe Ser Tyr Phe Gln Asp Leu Val Ile		
4210	4215	4220
Thr Leu Pro Phe Glu Leu Arg Lys His Lys Leu Ile Asp Val Ile Ser		
4225	4230	4235 4240
Met Tyr Arg Glu Leu Leu Lys Asp Leu Ser Lys Glu Ala Gln Glu Val		
4245	4250	4255
Phe Lys Ala Ile Gln Ser Leu Lys Thr Thr Glu Val Leu Arg Asn Leu		
4260	4265	4270
Gln Asp Leu Leu Gln Phe Ile Phe Gln Leu Ile Glu Asp Asn Ile Lys		
4275	4280	4285
Gln Leu Lys Glu Met Lys Phe Thr Tyr Leu Ile Asn Tyr Ile Gln Asp		
4290	4295	4300

Glu Ile Asn Thr Ile Phe Asn Asp Tyr Ile Pro Tyr Val Phe Lys Leu			
4305	4310	4315	4320
Leu Lys Glu Asn Leu Cys Leu Asn Leu His Lys Phe Asn Glu Phe Ile			
	4325	4330	4335
Gln Asn Glu Leu Gln Glu Ala Ser Gln Glu Leu Gln Gln Ile His Gln			
	4340	4345	4350
Tyr Ile Met Ala Leu Arg Glu Glu Tyr Phe Asp Pro Ser Ile Val Gly			
	4355	4360	4365
Trp Thr Val Lys Tyr Tyr Glu Leu Glu Glu Lys Ile Val Ser Leu Ile			
	4370	4375	4380
Lys Asn Leu Leu Val Ala Leu Lys Asp Phe His Ser Glu Tyr Ile Val			
4385	4390	4395	4400
Ser Ala Ser Asn Phe Thr Ser Gln Leu Ser Ser Gln Val Glu Gln Phe			
	4405	4410	4415
Leu His Arg Asn Ile Gln Glu Tyr Leu Ser Ile Leu Thr Asp Pro Asp			
	4420	4425	4430
Gly Lys Gly Lys Glu Lys Ile Ala Glu Leu Ser Ala Thr Ala Gln Glu			
	4435	4440	4445
Ile Ile Lys Ser Gln Ala Ile Ala Thr Lys Lys Ile Ile Ser Asp Tyr			
	4450	4455	4460
His Gln Gln Phe Arg Tyr Lys Leu Gln Asp Phe Ser Asp Gln Leu Ser			
4465	4470	4475	4480
Asp Tyr Tyr Glu Lys Phe Ile Ala Glu Ser Lys Arg Leu Ile Asp Leu			
	4485	4490	4495
Ser Ile Gln Asn Tyr His Thr Phe Leu Ile Tyr Ile Thr Glu Leu Leu			
	4500	4505	4510
Lys Lys Leu Gln Ser Thr Thr Val Met Asn Pro Tyr Met Lys Leu Ala			
	4515	4520	4525
Pro Gly Glu Leu Thr Ile Ile Leu			
	4530	4535	

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Xaa Pro  
1

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Lys	Tyr	Thr	Tyr	Asn	Tyr	Glu	Ala	Glu	Ser	Ser	Ser	Gly	Val	Pro	Gly
1				5					10					15	
Thr	Ala	Asp	Ser	Arg	Ser	Ala	Thr	Arg	Ile	Asn	Cys	Lys	Val	Glu	Leu
			20					25					30		
Glu	Val	Pro	Gln	Leu	Cys	Ser	Phe	Ile	Leu	Lys	Thr	Ser	Gln		
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala	Tyr	Asp	Phe	Asn	Tyr	Pro	Ile	Lys	Lys	Asp	Ser	Ser	Ser	Gln	Leu
1				5				10						15	
Leu	Ser	Val	Gln	Gln	Gly	Glu	Thr	Ile	Tyr	Ile	Leu	Asn	Lys	Asn	Ser
			20					25					30		
Ser	Gly	Trp	Trp	Asp	Gly	Leu	Val	Ile	Asp	Asp	Ser	Asn			
		35				40						45			

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Val	Tyr	Gly	Phe	Asn	Pro	Glu	Gly	Lys	Ala	Leu	Leu	Lys	Lys	Thr	Lys
1				5					10					15	
Asn	Ser	Glu	Glu	Phe	Ala	Ala	Ala	Met	Ser	Arg	Tyr	Glu	Leu	Lys	Leu
			20					25					30		
Ala	Ile	Pro	Glu	Gly	Lys	Gln	Val	Phe	Leu	Tyr	Pro	Glu			
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Leu	Tyr	Asp	Phe	Val	Ala	Ser	Gly	Asp	Asn	Thr	Leu	Ser	Ile	Thr	Lys
1				5					10					15	
Gly	Glu	Lys	Leu	Arg	Val	Leu	Gly	Tyr	Asn	His	Tyr	Asn	Gly	Glu	Trp
			20					25					30		
Cys	Glu	Ala	Gln	Thr	Lys	Asn	Gly	Gln	Gly	Trp	Val	Pro	Ser	Asn	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe	Leu	Pro	Phe	Ser	Tyr	Asn	Asn	Lys	Tyr	Gly	Met	Val	Ala	Gln	Val
1				5					10					15	
Thr	Gln	Thr	Leu	Lys	Leu	Glu	Asp	Thr	Pro	Lys	Ile	Asn	Ser	Arg	Phe
			20					25					30		
Phe	Gly	Glu	Gly	Thr	Lys	Lys	Met	Gly	Leu	Ala	Phe				
		35					40								

(2) INFORMATION FOR SEO ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Phe Asp Tyr Lys Ala Gln Arg Glu Asp Glu Leu Thr Phe Thr Lys  
1 5 10 15  
Ser Ala Ile Ile Gln Asn Val Glu Lys Gln Glu Gly Gly Trp Trp Arg  
20 25 30  
Gly Asp Tyr Gly Gly Lys Lys Gln Leu Trp Phe  
35 40

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Phe	Leu	Pro	Phe	Ser	Tyr	Asn	Asn	Lys	Tyr	Gly	Met	Val	Ala	Gln	Val
1				5					10					15	
Thr	Gln	Thr	Leu	Lys	Leu	Glu	Asp	Thr	Pro	Lys	Ile	Asn	Ser	Arg	Phe
			20					25					30		
Phe	Gly	Glu	Gly	Thr	Lys	Lys	Met	Gly	Leu	Ala	Phe	Glu			
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu Gly Phe Glu Lys  
1 5 10 15



Gly Glu Gln Leu Arg Ile Leu Glu Gln Ser Gly Glu Trp Trp Lys Ala  
 20 25 30

Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro Phe Asn  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Tyr Thr Tyr Leu Ile Leu Arg Val Ile Gly Asn Met Gly Gln Thr Met  
 1 5 10 15

Glu Gln Leu Thr Pro Glu Leu Lys Ser Ser Ile Leu Lys Cys Val Gln  
 20 25 30

Ser Thr Lys Pro Ser Leu Met Ile Gln Lys Ala Ala Ile Gln Ala Leu  
 35 40 45

Arg Lys Met Glu Pro Lys Asp Lys Asp Gln Glu Val Leu Leu  
 50 55 60

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Val Val Ala Leu Phe Asp Tyr Ala Ala Val Asn Asp Arg Asp Leu Gln  
 1 5 10 15

Val Leu Lys Gly Glu Lys Leu Gln Val Leu Arg Ser Thr Gly Asp Trp  
 20 25 30

Trp Leu Ala Arg Ser Leu Val Thr Gly Arg Glu Gly Tyr Val Pro Ser  
 35 40 45

Asn Phe Val Ala Pro  
 50

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Phe Gly Phe Ala Ser Ala Asp Leu Ile Glu Ile Gly Leu Glu Gly  
1 5 10 15

Lys Gly Phe Glu Pro Thr Leu Glu Ala Leu Phe Gly Lys Gln Gly Phe  
20 25 30

Phe Pro Asp Ser Val Asn Lys Ala Leu Tyr Trp Val Asn Gly Gln Val  
35 40 45

Pro Asp  
50

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Tyr Asp Phe Ala Ala Glu Asn Pro Asp Glu Leu Thr Phe Asn Glu  
1 5 10 15

Gly Ala Val Val Thr Val Ile Asn Lys Ser Asn Pro Asp Trp Trp Glu  
20 25 30

Gly Glu Leu Asn Gly Gln Arg Gly Val Phe Pro Ala Ser Tyr Val Glu  
35 40 45

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe	Gly	Tyr	Thr	Lys	Asp	Asp	Lys	His	Glu	Gln	Asp	Met	Val	Asn	Gly
1				5					10					15	
Ile	Met	Leu	Ser	Val	Glu	Lys	Leu	Ile	Lys	Asp	Leu	Lys	Ser	Lys	Glu
			20					25					30		
Val	Pro	Glu	Ala	Arg	Ala	Tyr	Leu	Arg	Ile	Leu	Gly	Glu	Glu		
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Tyr	Asp	Tyr	Lys	Lys	Glu	Glu	Glu	Asp	Ile	Asp	Leu	His	Leu	Gly	Asp
1			5						10					15	
Ile	Leu	Thr	Val	Asn	Lys	Gly	Ser	Leu	Val	Ala	Leu	Gly	Phe	Ser	Asp
			20					25					30		
Gly	Gln	Glu	Ala	Lys	Pro	Glu	Glu	Ile	Gly	Trp	Leu	Asn	Gly	Tyr	Asn
		35					40					45			
Glu															

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Phe	Asp	Tyr	His	Gln	Phe	Val	Asp	Glu	Thr	Asn	Asp	Lys	Ile	Arg	Glu
1				5					10					15	
Val	Thr	Gln	Arg	Leu	Asn	Gly	Glu	Ile	Gln	Ala	Leu	Glu	Leu	Pro	Gln
			20					25					30		
Lys	Ala	Glu	Ala	Leu	Lys	Leu	Phe	Leu	Glu	Glu	Thr	Lys	Ala	Thr	Val
		35					40					45			
Ala	Val	Tyr	Leu												
	50														

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Tyr	Asp	Tyr	Gln	Glu	Lys	Ser	Pro	Arg	Glu	Val	Thr	Met	Lys	Lys	Gly
1				5					10					15	
Asp	Ile	Leu	Thr	Leu	Leu	Asn	Ser	Thr	Asn	Lys	Asp	Trp	Trp	Lys	Val
			20					25					30		
Glu	Val	Asn	Asp	Arg	Gln	Gly	Phe	Val	Pro	Ala	Ala	Tyr	Val		
		35					40						45		

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Tyr	Asp	Met	Asp	Ile	Gln	Gln	Glu	Leu	Gln	Arg	Tyr	Leu	Ser	Leu	Val
1				5					10					15	
Gly	Gln	Val	Tyr	Ser	Thr	Leu	Val	Thr	Tyr	Ile	Ser	Asp	Trp	Trp	Thr
			20					25					30		
Leu	Ala	Ala	Lys	Asn	Leu	Thr	Asp	Phe	Ala	Glu	Gln	Tyr	Ser	Ile	Gln
			35				40						45		
Asp	Trp	Ala													
			50												

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Phe Asp Tyr Lys Ala Gln Arg Glu Asp Glu Leu Thr Phe Thr Lys Ser  
1 5 10 15  
Ala Ile Ile Gln Asn Val Glu Lys Gln Asp Gly Gly Trp Trp Arg Gly  
20 25 30  
Asp Tyr Gly Gly Lys Lys Gln Leu Trp Phe Pro Ser Asn Tyr Val Glu  
35 40 45  
Glu Met Ile  
50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Tyr Asp Met Asp Ile Gln Gln Glu Leu Gln Arg Tyr Leu Ser Leu Val  
1 5 10 15  
Gly Gln Val Tyr Ser Thr Leu Val Thr Tyr Ile Ser Asp Trp Trp Thr  
20 25 30  
Leu Ala Ala Lys Asn Leu Thr Asp Phe Ala Glu Gln Tyr Ser Ile Gln  
35 40 45  
Asp Trp Ala Lys Arg Met Lys  
50 55

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Gln Asp Tyr Glu Pro Arg Leu Thr Asp Glu Ile Arg Ile Ser Leu  
1 5 10 15  
Gly Glu Lys Val Lys Ile Leu Ala Thr His Thr Asp Gly Trp Cys Leu  
20 25 30

Val Glu Lys Cys Asn Thr Arg Lys Gly Thr Ile His Val Ser Val Asp  
 35 40 45

Asp Lys Arg Tyr Leu  
 50

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu Thr Phe Thr Lys Gly  
 1 5 10 15

Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly Asp Trp Trp Glu Ala  
 20 25 30

Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile Pro Ser Asn Tyr Val  
 35 40 45

Ala

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Thr Tyr Asp Phe Ser Phe Lys Ser Ser Val Ile Thr Leu Asn Thr Asn  
 1 5 10 15

Ala Glu Leu Phe Asn Gln Ser Asp Ile Val Ala His Leu Leu Ser Ser  
 20 25 30

Ser Ser Ser Val Ile Asp Ala Leu Gln Tyr Lys Leu Glu  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp	Phe	Asn	Tyr	Pro	Ile	Lys	Lys	Asp	Ser	Ser	Ser	Gln	Leu	Leu	Ser
1				5				10					15		
Val	Gln	Gln	Gly	Glu	Thr	Ile	Tyr	Ile	Leu	Asn	Lys	Asn	Ser	Ser	Gly
			20					25					30		
Trp	Trp	Asp	Gly	Leu	Val	Ile	Asp	Asp	Ser	Asn	Gly	Lys	Val	Asn	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys	Tyr	Asp	Phe	Asn	Ser	Ser	Met	Leu	Tyr	Ser	Thr	Ala	Lys	Gly	Ala
1				5				10					15		
Val	Asp	His	Lys	Leu	Ser	Leu	Glu	Ser	Leu	Thr	Ser	Tyr	Phe	Ser	Ile
			20					25					30		
Glu	Ser	Ser	Thr	Lys	Gly	Asp	Val	Lys	Gly	Ser	Val	Leu	Ser	Arg	Glu
		35					40					45			
Tyr															

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Glu	Pro	Tyr	Val	Ala	Ile	Lys	Ala	Tyr	Thr	Ala	Val	Glu	Gly	Asp	Glu
1				5				10					15		
Val	Ser	Leu	Leu	Glu	Gly	Glu	Ala	Val	Glu	Val	Ile	His	Lys	Leu	Leu
			20					25					30		

Asp Gly Trp Trp Val Ile Arg Lys Asp Asp Val Thr Gly Tyr Phe Pro  
 35 40 45

Ser Met Tyr Leu  
 50

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Trp Asp Phe Leu Lys Leu Asp Val Thr Thr Ser Ile Gly Arg Arg  
 1 5 10 15

Gln His Leu Arg Val Ser Thr Ala Phe Val Tyr Thr Lys Asn Pro Asn  
 20 25 30

Gly Tyr Ser Phe Ser Ile Pro Val Lys Val Leu Ala Asp Lys Phe Ile  
 35 40 45

Thr Pro Gly Leu Lys Leu  
 50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Leu Tyr Asp Phe Lys Ala Glu Lys Ala Asp Glu Leu Thr Thr Tyr Val  
 1 5 10 15

Gly Glu Asn Leu Phe Ile Cys Ala His His Asn Cys Glu Trp Phe Ile  
 20 25 30

Ala Lys Pro Ile Gly Arg Leu Gly Gly Pro Gly Leu Val Pro Val Gly  
 35 40 45

Phe Val Ser Ile Ile Asp Ile  
 50 55



(2) INFORMATION FOR SEO ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Val	Leu	Tyr	Asp	Tyr	Val	Asn	Lys	Tyr	His	Trp	Glu	His	Thr	Gly	Leu
1				5					10					15	
Thr	Leu	Arg	Glu	Val	Ser	Ser	Lys	Leu	Arg	Arg	Asn	Leu	Gln	Asn	Asn
			20					25					30		
Ala	Glu	Trp	Val	Tyr	Gln	Gly	Ala	Ile	Arg	Gln	Ile	Asp	Asp	Ile	
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Val	Leu	Tyr	Asp	Phe	Lys	Ala	Glu	Lys	Ala	Asp	Glu	Leu	Thr	Thr	Tyr
1				5					10					15	
Val	Gly	Glu	Asn	Leu	Phe	Ile	Cys	Ala	His	His	Asn	Cys	Glu	Trp	Phe
			20					25					30		
Ile	Ala	Lys	Pro	Ile	Gly	Arg	Leu								
		35					40								

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys Pro Gly Ile Tyr Thr Arg Glu Glu Leu Cys Thr Met Phe Ile Arg  
1 5 10 15

Glu Val Gly Thr Val Leu Ser Gln Val Tyr Ser Lys Val His Asn Gly  
 20 25 30

Ser Glu Ile Leu Phe Ser Tyr Phe Gln Asp Leu  
 35 40

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Leu Phe Gly Phe Val Pro Glu Thr Lys Glu Glu Leu Gln Val Met Pro  
 1 5 10 15

Gly Asn Ile Val Phe Val Leu Lys Lys Gly Asn Asp Asn Trp Ala Thr  
 20 25 30

Val Met Phe Asn Gly Gln Lys Gly Leu Val Pro Cys Asn Tyr Leu Glu  
 35 40 45

Pro Val Glu Leu  
 50

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Lys Pro Gly Ile Tyr Thr Arg Glu Glu Leu Cys Thr Met Phe Ile  
 1 5 10 15

Arg Glu Val Gly Thr Val Leu Ser Gln Val Tyr Ser Lys Val His Asn  
 20 25 30

Gly Ser Glu Ile Leu Phe Ser Tyr Phe Gln Asp  
 35 40

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Ala	Lys	Phe	Asp	Tyr	Val	Ala	Gln	Gln	Glu	Gln	Glu	Leu	Asp	Ile	Lys
1				5					10					15	
Lys	Asn	Glu	Arg	Leu	Trp	Leu	Leu	Asp	Asp	Ser	Lys	Ser	Trp	Trp	Arg
			20					25					30		
Val	Arg	Asn	Ser	Met	Asn	Lys	Thr	Gly	Phe	Val	Pro	Ser	Asn	Tyr	Val
		35					40						45		
Glu	Arg	Lys	Asn												
			50												

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 85 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Trp	Tyr	His	Ala	Ser	Leu	Thr	Arg	Ala	Gln	Ala	Glu	His	Met	Leu	Met
1				5					10					15	
Arg	Val	Pro	Arg	Asp	Gly	Ala	Phe	Leu	Val	Arg	Lys	Arg	Asn	Glu	Pro
			20					25					30		
Asn	Ser	Tyr	Ala	Ile	Ser	Phe	Arg	Ala	Glu	Gly	Lys	Ile	Lys	His	Cys
			35				40					45			
Arg	Val	Gln	Gln	Glu	Gly	Thr	Val	Met	Leu	Gly	Asn	Ser	Glu	Phe	Asp
			50				55				60				
Ser	Leu	Val	Asp	Leu	Ile	Ser	Tyr	Tyr	Glu	Lys	His	Pro	Leu	Tyr	Arg
			65			70				75				80	
Lys	Met	Lys	Leu	Arg											
				85											

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 106 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe	Phe	Gly	Glu	Gly	Thr	Lys	Lys	Met	Gly	Leu	Ala	Phe	Glu	Ser	Thr	
1				5					10					15		
Lys	Ser	Thr	Ser	Pro	Pro	Lys	Gln	Ala	Glu	Ala	Val	Leu	Lys	Thr	Leu	
			20					25					30			
Gln	Glu	Leu	Lys	Lys	Leu	Thr	Ile	Ser	Glu	Gln	Asn	Ile	Gln	Arg	Ala	
		35					40					45				
Asn	Leu	Phe	Asn	Lys	Leu	Val	Thr	Glu	Leu	Arg	Gly	Leu	Ser	Asp	Glu	
	50					55					60					
Ala	Val	Thr	Ser	Leu	Leu	Pro	Gln	Leu	Ile	Glu	Val	Ser	Ser	Pro	Ile	
65					70					75					80	
Thr	Leu	Gln	Ala	Leu	Val	Gln	Cys	Gly	Gln	Pro	Cys	Ser	Thr	His	Ile	
				85					90					95		
Leu	Gln	Trp	Leu	Lys	Arg	Val	His	Ala	Asn							
			100						105							

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Trp	Phe	His	Gly	Lys	Ile	Ser	Lys	Gln	Glu	Ala	Tyr	Asn	Leu	Leu	Met	
1				5					10					15		
Thr	Val	Gly	Gln	Ala	Cys	Ser	Phe	Leu	Val	Arg	Pro	Ser	Asp	Asn	Thr	
			20					25					30			
Pro	Gly	Asp	Tyr	Ser	Leu	Tyr	Phe	Arg	Thr	Ser	Glu	Asn	Ile	Gln	Arg	
		35					40					45				
Phe	Lys	Ile	Cys	Pro	Thr	Pro	Asn	Asn	Gln	Phe	Met	Met	Gly	Gly	Arg	
	50						55				60					
Tyr	Tyr	Asn	Ser	Ser	Ile	Gly	Asp	Ile	Ile	Asp	His	Tyr	Arg	Lys	Glu	
65					70					75					80	
Gln	Ile	Val	Glu	Gly	Tyr	Tyr	Leu	Lys	Glu	Pro						
				85					90							

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ile Met Leu Ser Val Glu Lys Leu Ile Lys Asp Leu Lys Ser Lys Glu  
1                      5                      10                      15  
Val Pro Glu Ala Arg Ala Tyr Leu Arg Ile Leu Gly Glu Glu Leu Gly  
                    20                      25                      30  
Phe Ala Ser Leu His Asp Leu Gln Leu Leu Gly Lys Leu Leu Leu Met  
                    35                      40                      45  
Gly Ala Arg Thr Leu Gln Gly Ile Pro Gln Met Ile Gly Glu Val Ile  
50                      55                      60  
Arg Lys Gly Ser Lys Asn Asp Phe Phe Leu His Tyr Ile Phe Met Glu  
65                      70                      75                      80  
Asn Ala Phe Glu Leu Pro Thr Gly Ala Gly Leu Gln Leu  
                    85                      90

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Trp Phe His Gly Lys Ile Ser Lys Gln Glu Ala Tyr Asn Leu Leu Met  
1                      5                      10                      15  
Thr Val Gly Gln Ala Cys Ser Phe Leu Val Arg Pro Ser Asp Asn Thr  
                    20                      25                      30  
Pro Gly Asp Tyr Ser Leu Tyr Phe Arg Thr Ser Glu Asn Ile Gln Arg  
                    35                      40                      45  
Phe Lys Ile Cys Pro Thr Pro Asn Asn Gln Phe Met Met Gly Gly Arg  
50                      55                      60  
Tyr Tyr Asn Ser Ser Ile Gly Asp Ile Ile Asp His Tyr Arg Lys Glu  
65                      70                      75                      80

Gln Ile Val Glu Gly Tyr Tyr Leu Lys  
85

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Tyr	Phe	His	Lys	Leu	Asn	Ile	Pro	Lys	Leu	Asp	Phe	Ser	Ser	Gln	Ala	1	5	10	15
Asp	Leu	Arg	Asn	Glu	Ile	Lys	Thr	Leu	Leu	Lys	Ala	Gly	His	Ile	Ala	20	25	30	
Trp	Thr	Ser	Ser	Gly	Lys	Gly	Ser	Trp	Lys	Trp	Ala	Cys	Pro	Arg	Phe	35	40	45	
Ser	Asp	Glu	Gly	Thr	His	Glu	Ser	Gln	Ile	Ser	Phe	Thr	Ile	Glu	Gly	50	55	60	
Pro	Leu	Thr	Ser	Phe	Gly	Leu	Ser	Asn	Lys	Ile	Asn	Ser				65	70	75	

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Trp	Tyr	Trp	Gly	Asp	Ile	Ser	Arg	Glu	Glu	Val	Asn	Glu	Lys	Leu	Arg	1	5	10	15
Asp	Thr	Pro	Asp	Gly	Thr	Phe	Leu	Val	Arg	Asp	Ala	Ser	Ser	Lys	Ile	20	25	30	
Gln	Gly	Asp	Tyr	Leu	Thr	Leu	Arg	Lys	Gly	Gly	Asn	Asn	Lys	Leu	Ile	35	40	45	
Lys	Val	Phe	His	Arg	Asp	Gly	Lys	Tyr	Gly	Phe	Ser	Glu	Pro	Leu	Thr	50	55	60	

Phe Cys Ser Val Val Asp Leu Ile Thr His Tyr Arg His Glu Ser Leu  
65 70 75 80

Ala Gln Tyr Asn Ala Lys Leu Asp Thr Arg Leu Leu Tyr Pro Val Ser  
85 90 95

Lys Tyr

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Phe Phe Ser Ala Gln Pro Phe Glu Ile Thr Ala Ser Thr Asn Asn Glu  
1 5 10 15

Gly Asn Leu Lys Val Arg Phe Pro Leu Arg Leu Thr Gly Lys Ile Asp  
20 25 30

Phe Leu Asn Asn Tyr Ala Leu Phe Leu Ser Pro Ser Ala Gln Gln Ala  
35 40 45

Ser Trp Gln Val Ser Ala Arg Phe Asn Gln Tyr Lys Tyr Asn Gln Asn  
50 55 60

Phe Ser Ala Gly Asn Asn Glu Asn Ile Met Glu Ala His Val Gly Ile  
65 70 75 80

Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn Ile Pro Leu Thr Ile Pro  
85 90 95

Glu Met Arg Leu  
100

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Trp Phe His Gly Lys Leu Gly Ala Gly Arg Asp Gly Arg His Ile Ala  
1 5 10 15

Glu Arg Leu Leu Thr Glu Tyr Cys Ile Glu Thr Gly Ala Pro Asp Gly  
                   20                                  25                                  30  
 Ser Phe Leu Val Arg Glu Ser Glu Thr Phe Val Gly Asp Tyr Thr Leu  
                   35                                  40                                  45  
 Ser Phe Trp Arg Asn Gly Lys Val Gln His Cys Arg Ile His Ser Arg  
                   50                                  55                                  60  
 Gln Asp Ala Gly Thr Pro Lys Phe Phe Leu Thr Asp Asn Leu Val Phe  
                   65                                  70                                  75                                  80  
 Asp Ser Leu Tyr Asp Leu Ile Thr His Tyr Gln Gln Val Pro Leu Arg  
                                   85                                  90                                  95  
 Cys Asn Glu Phe Glu Met Arg Leu Ser Glu  
                   100                                  105

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Phe Pro Gly Lys Pro Gly Ile Tyr Thr Arg Glu Glu Leu Cys Thr Met  
 1                                  5                                  10                                  15  
 Phe Ile Arg Glu Val Gly Thr Val Leu Ser Gln Val Tyr Ser Lys Val  
                   20                                  25                                  30  
 His Asn Gly Ser Glu Ile Leu Phe Ser Tyr Phe Gln Asp Leu Val Ile  
                   35                                  40                                  45  
 Thr Leu Pro Phe Glu Leu Arg Lys His Lys Leu Ile Asp Val Ile Ser  
                   50                                  55                                  60  
 Met Tyr Arg Glu Leu Leu Lys Asp Leu Ser Lys Glu Ala Gln Glu Val  
                   65                                  70                                  75                                  80  
 Phe Lys Ala Ile Gln Ser Leu Lys Thr Thr Glu  
                                   85                                  90

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 amino acids
- (B) TYPE: amino acid



- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Val	Ser	Asp	Gly	Ile	Ala	Ala	Leu	Asp	Leu	Asn	Ala	Val	Ala	Asn	Lys	1	5	10	15
Ile	Ala	Asp	Phe	Glu	Leu	Pro	Thr	Ile	Ile	Val	Pro	Glu	Gln	Thr	Ile	20	25	30	
Glu	Ile	Pro	Ser	Ile	Lys	Phe	Ser	Val	Pro	Ala	Gly	Ile	Val	Ile	Pro	35	40	45	
Ser	Phe	Gln	Ala	Leu	Thr	Ala	Arg	Phe	Glu	Val	Asp	Ser	Pro	Val	Tyr	50	55	60	
Asn	Ala	Thr	Trp	Ser	Ala	Ser	Leu	Lys	Asn	Lys	Ala	Asp	Tyr	Val	Glu	65	70	75	80
Thr	Val	Leu	Asp	Ser	Thr	Cys	Ser	Ser	Thr	Val	Gln	Phe	Leu	Glu	Tyr	85	90	95	
Glu	Leu	Asn	Val	Leu	Gly	Thr	His	Lys	Ile	Glu	Asp	Gly	Thr	Leu	Ala	100	105	110	
Ser	Lys	Thr	Lys	Gly	Thr	Leu	Ala	His	Arg	Asp	Phe	Ser	Ala	Glu	Tyr	115	120	125	
Glu	Glu	Asp	Gly	Lys	Phe	Glu	Gly	Leu	Gln	Glu	Trp	Glu	Gly	Lys	Ala	130	135	140	
His	Leu	Asn	Ile	Lys	Ser	Pro	Ala	Phe	Thr	Asp	Leu	His	Leu	Arg	Tyr	145	150	155	160
Gln	Lys	Asp	Lys	Lys	Gly	Ile	Ser	Thr	Ser	Ala	Ala	Ser	Pro	Ala	Val	165	170	175	
Gly	Thr	Val	Gly	Met	Asp	Met	Asp	Glu	Asp	Asp	Asp	Phe	Ser	Lys	Trp	180	185	190	
Asn	Phe	Tyr	Tyr	Ser	Pro	Gln	Ser	Ser	Pro	Asp						195	200		

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 214 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly  
1 5 10 15  
Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro  
20 25 30  
Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu Arg His Glu  
35 40 45  
Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile  
50 55 60  
Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe Leu Lys Gly  
65 70 75 80  
Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala  
85 90 95  
Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn Tyr Val His  
100 105 110  
Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn Leu Val Cys  
115 120 125  
Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr  
130 135 140  
Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu  
145 150 155 160  
Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe  
165 170 175  
Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val Pro Tyr Pro  
180 185 190  
Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg Gly Tyr Arg  
195 200 205  
Met Pro Cys Pro Pro Glu  
210

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr Trp Asn Gly  
1 5 10 15  
Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly Thr Met Ser Pro  
20 25 30  
Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys Leu Lys His Asp  
35 40 45  
Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile  
50 55 60  
Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp Phe Leu Lys Asp  
65 70 75 80  
Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val Asp Met Ala Ala  
85 90 95  
Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn Tyr Ile His  
100 105 110  
Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn Gly Leu Ile Cys  
115 120 125  
Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr  
130 135 140  
Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu  
145 150 155 160  
Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe  
165 170 175  
Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val Pro Tyr Pro  
180 185 190  
Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg Gly Tyr Arg  
195 200 205  
Met Pro Cys Pro Gln  
210

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 213 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Ala Thr Tyr Asn Lys  
1                   5                   10                   15

His Thr Lys Val Ala Val Lys Thr Met Lys Pro Gly Ser Met Ser Val  
20                   25                   30

Glu Ala Phe Leu Ala Glu Ala Asn Val Met Lys Thr Leu Gln His Asp  
35                   40                   45

Lys Leu Val Lys Leu His Ala Val Val Thr Lys Glu Pro Ile Tyr Ile  
50                   55                   60

Ile Thr Glu Phe Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser  
65                   70                   75                   80

Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys Leu Ile Asp Phe Ser Ala  
85                   90                   95

Gln Ile Ala Glu Gly Met Ala Phe Ile Glu Gln Arg Asn Tyr Ile His  
100                   105                   110

Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Ala Ser Leu Val Cys  
115                   120                   125

Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr  
130                   135                   140

Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu  
145                   150                   155                   160

Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys Ser Asp Val Trp Ser Phe  
165                   170                   175

Gly Ile Leu Leu Met Glu Ile Val Thr Tyr Gly Arg Ile Pro Tyr Pro  
180                   185                   190

Gly Met Ser Asn Pro Glu Val Ile Arg Ala Leu Glu Arg Gly Tyr Arg  
195                   200                   205

Met Pro Arg Pro Glu  
210

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Gly Ala Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn  
1 5 10 15  
Ser Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val  
20 25 30  
Gln Ala Phe Leu Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp  
35 40 45  
Lys Leu Val Arg Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr  
50 55 60  
Ile Ile Thr Glu Tyr Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys  
65 70 75 80  
Ser Asp Glu Gly Gly Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser  
85 90 95  
Ala Gln Ile Ala Glu Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile  
100 105 110  
His Arg Asp Leu Arg Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met  
115 120 125  
Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu  
130 135 140  
Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro  
145 150 155 160  
Glu Ala Ile Asn Phe Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser  
165 170 175  
Phe Gly Ile Leu Leu Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr  
180 185 190  
Pro Gly Arg Thr Asn Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr  
195 200 205  
Arg Met Pro Arg Val Glu Asn Cys Pro Asp  
210 215

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- 142-

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Arg Lys Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn  
1 5 10

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Gly Thr Leu Ala His Arg Asp Phe Ser Ala Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Asp Lys Val Ala Ile Lys Thr Ile Arg Glu Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Asp Leu Asn Ala Val Ala Asn Lys Ile Ala Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Thr Ser Leu Arg Ala Pro Thr Met Pro Pro Pro Leu Pro Pro Val Pro  
1 5 10 15  
Pro Gln Pro Ala Arg Arg Gln Ser Arg Arg Leu Pro Ala Ser Pro Val  
20 25 30  
Ile Ser

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro Thr Val Thr Pro Val  
1 5 10 15  
Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro Thr Glu Gln Arg Pro  
20 25 30  
Gly Val Gln Glu  
35

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
Ser Asp Ala Glu Gly Thr Ala Val Ala Pro Pro Thr Ile Thr Pro Ile
1           5           10           15

Pro Ser Leu Glu Ala Pro Ser Glu Gln Ala Pro Thr Glu Gln Arg Pro
          20           25           30

Gly Val Gln Glu
          35
```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
Ser Asp Ala Glu Trp Thr Ala Phe Val Pro Pro Asn Val Ile Leu Ala
1           5           10           15

Pro Ser Leu Glu Ala Phe Phe Glu Gln Ala Leu Thr Glu Glu Thr Pro
          20           25           30

Gly Val Gln Asp
          35
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
Leu Val Thr Glu Ser Ser Val Leu Ala Thr Leu Thr Val Val Pro Asp
1           5           10           15

Pro Ser Thr Glu Ala Ser Ser Glu Glu Ala Pro Thr Glu Gln Ser Pro
          20           25           30

Gly Val Gln Asp
          35
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Pro Val Met Glu Ser Thr Leu Leu Thr Thr Pro Thr Val Val Pro Val  
1                      5                      10                      15  
  
Pro Ser Thr Glu Leu Pro Ser Glu Glu Ala Pro Thr Glu Asn Ser Thr  
                    20                      25                      30  
  
Gly Val Gln Asp  
                    35

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Pro Val Thr Glu Ser Ser Val Leu Thr Thr Pro Thr Val Ala Pro Val  
1                      5                      10                      15  
  
Pro Ser Thr Glu Ala Pro Ser Glu Gln Ala Pro Pro Glu Lys Ser Pro  
                    20                      25                      30  
  
Val Val Gln Asp  
                    35

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ser Glu Thr Glu Ser Gly Val Leu Glu Thr Pro Thr Val Val Pro Glu  
1                      5                      10                      15

Pro Ser Met Glu Ala His Ser Glu Ala Ala Pro Thr Glu Gln Thr Pro  
 20 25 30

Val Val Arg Arg Gln  
 35

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Pro Lys Asp Ala Thr Arg Phe Lys His Leu Arg Lys Tyr Thr Tyr Asn  
 1 5 10 15

Tyr Glu Ala Glu Ser Ser Ser Gly Val Pro Gly Thr Ala Asp Ser Arg  
 20 25 30

Ser Ala Thr Arg Ile  
 35

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Pro Lys Asp Ala Thr Arg Phe Lys His Leu Arg Lys Tyr Thr Tyr Asn  
 1 5 10 15

Tyr Glu Ala Glu Ser Ser Ser Gly Val Pro Gly Thr Ala Asp Ser Arg  
 20 25 30

Ser Ala Thr Arg Ile  
 35

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```

Pro Lys Asp Ala Ser Gln Arg Arg Arg Ser Leu Glu Pro Ala Glu Asn
1          5          10          15
Val His Gly Ala Gly Gly Gly Ala Phe Pro Ala Ser Gln Thr Pro Ser
          20          25          30
Lys Pro

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Asp Lys Glu Ala Thr Lys Leu Thr Glu Glu Arg Asp Gly Ser Leu Asn  
1 5 10 15

Gln Ser Ser Gly Tyr Arg Tyr Gly Thr Asp Pro Thr Pro Gln His Tyr  
20 25 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Ile Gln Asn Tyr His Thr Phe Leu Ile Tyr Ile Thr Glu Leu Leu Lys  
1               5                     10                         15

Lys Leu Gln Ser Thr Thr Val Met Asn Pro Tyr Met Lys Leu Ala Pro  
          20                     25                         30

Gly Glu Leu Thr Ile Ile Leu  
          35

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ala Phe Leu Glu Asp
1           5           10           15

Tyr Phe Thr Ser Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
          20           25           30

```

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp
1           5           10           15

Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
          20           25           30

```

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Pro Glu Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp
1           5           10           15

Phe Tyr Thr Ala Thr Glu Ser Gln Tyr Gln Gln Gln Pro
          20           25

```

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val Leu Asp Asp  
1 5 10 15

Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro  
20 25

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp  
1 5 10 15

Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro  
20 25

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Pro Xaa Xaa Xaa Xaa Pro  
1 5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Pro Asp Phe Arg Leu Pro Glu Ile Ala Ile Pro Glu Phe Ile Ile Pro  
1 5 10 15

Thr Leu Asn Leu Asn Asp Phe Gln Val Pro Asp Leu His Ile Pro Glu  
20 25 30

Phe Gln Leu Pro His Ile Ser His  
35 40

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Pro Gln Asn Ala Lys Leu Lys Ile Lys Arg Pro Val Lys Val Gln Pro  
1 5 10 15

Ile Ala Arg Val Trp Tyr  
20

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Pro Asp Phe Arg Leu Pro Glu Ile Ala Ile Pro Glu Phe Ile Ile Pro  
1 5 10 15

Thr Leu Asn Leu Asn Asp  
20

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Asn Asp Phe Gln Val Pro Asp Leu His Ile Pro Glu Phe Gln Leu Pro  
1 5 10 15

His Ile Ser His Thr Ile  
20

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Pro Ser Leu Glu Leu Pro Val Leu His Val Pro Arg Asn Leu Lys Leu  
1 5 10 15  
Ser Leu Pro His Phe Lys  
20

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Met Ala Ser Gly Arg Ala Arg Cys Thr Arg Lys Leu Arg Asn Trp Val  
1 5 10 15  
Val Glu Gln Val Glu Ser Gly Gln Phe Pro Gly Val Cys Trp Asp Asp  
20 25 30  
Thr Ala Lys Thr Met Phe Arg Ile Pro Trp Lys His Ala Gly Lys Gln  
35 40 45  
Asp Phe Arg Glu Ser Gln Asp Ala Ala Phe Phe Lys Ala Trp Ala Ile  
50 55 60  
Phe Lys Gly Lys Tyr Lys Glu Gly Asp Lys Glu Val Pro Glu Arg Gly  
65 70 75 80  
Arg Met Asp Val Ala Glu Pro Tyr Lys Val Tyr Gln Leu Leu Pro Pro  
85 90 95  
Gly Ile Val Ser Gly Gln Pro Gly Thr Gln Lys Val Pro Ser Lys Arg  
100 105 110  
Gln His Ser Ser Val Ser Ser Glu Arg Lys Glu Glu Asp Ala Met Gln  
115 120 125



Asn	Cys	Thr	Leu	Ser	Pro	Ser	Val	Leu	Gln	Asp	Ser	Leu	Asn	Asn	Glu	130	135	140
Glu	Gly	Ala	Ser	Gly	Gly	Ala	Val	His	Ser	Asp	Ile	Gly	Ser	Ser	Ser	145	150	155
Ser	Ser	Ser	Ser	Pro	Glu	Pro	Gln	Glu	Val	Thr	Asp	Thr	Thr	Glu	Ala	165	170	175
Pro	Phe	Gln	Gly	Asp	Gln	Arg	Ser	Leu	Glu	Phe	Leu	Leu	Pro	Pro	Glu	180	185	190
Pro	Asp	Tyr	Ser	Leu	Leu	Leu	Thr	Phe	Ile	Tyr	Asn	Gly	Arg	Val	Val	195	200	205
Gly	Glu	Ala	Gln	Val	Gln	Ser	Leu	Asp	Cys	Arg	Leu	Val	Ala	Glu	Pro	210	215	220
Ser	Gly	Ser	Glu	Ser	Ser	Met	Glu	Gln	Val	Leu	Phe	Pro	Lys	Pro	Gly	225	230	235
Pro	Glu	Pro	Thr	Gln	Arg	Leu	Leu	Ser	Gln	Leu	Glu	Arg	Gly	Ile	Leu	245	250	255
Val	Ala	Ser	Asn	Pro	Arg	Gly	Leu	Phe	Val	Gln	Arg	Leu	Cys	Pro	Ile	260	265	270
Pro	Ile	Ser	Trp	Asn	Ala	Pro	Gln	Ala	Pro	Pro	Gly	Pro	Gly	Pro	His	275	280	285
Leu	Leu	Pro	Ser	Asn	Glu	Cys	Val	Glu	Leu	Phe	Arg	Thr	Ala	Tyr	Phe	290	295	300
Cys	Arg	Asp	Leu	Val	Arg	Tyr	Phe	Gln	Gly	Leu	Gly	Pro	Pro	Pro	Lys	305	310	315
Phe	Gln	Val	Thr	Leu	Asn	Phe	Trp	Glu	Glu	Ser	His	Gly	Ser	Ser	His	325	330	335
Thr	Pro	Gln	Asn	Leu	Ile	Thr	Val	Lys	Met	Glu	Gln	Ala	Phe	Ala	Arg	340	345	350
Tyr	Leu	Lys	Met	Glu	Gln	Ala	Phe	Ala	Arg	Tyr	Leu	Leu	Glu	Gln	Thr	355	360	365
Pro	Glu	Gln	Gln	Ala	Ala	Ile	Leu	Ser	Leu	Val						370	375	

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 383 amino acids

(B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Val	Ser	Leu	Val	Cys	Pro	Lys	Asp	Ala	Thr	Arg	Phe	Lys	His	Leu	Arg	1	5	10	15
Lys	Tyr	Thr	Tyr	Asn	Tyr	Glu	Ala	Glu	Ser	Ser	Ser	Gly	Val	Pro	Gly	20	25	30	
Thr	Ala	Asp	Ser	Arg	Ser	Ala	Thr	Arg	Ile	Asn	Cys	Lys	Val	Glu	Leu	35	40	45	
Glu	Val	Pro	Gln	Leu	Cys	Ser	Phe	Ile	Leu	Lys	Thr	Ser	Gln	Cys	Thr	50	55	60	
Leu	Lys	Glu	Val	Tyr	Gly	Phe	Asn	Pro	Glu	Gly	Lys	Ala	Leu	Leu	Lys	65	70	75	80
Lys	Thr	Lys	Asn	Ser	Glu	Glu	Phe	Ala	Ala	Ala	Met	Ser	Arg	Tyr	Glu	85	90	95	
Leu	Lys	Leu	Ala	Ile	Pro	Glu	Gly	Lys	Gln	Val	Phe	Leu	Tyr	Pro	Glu	100	105	110	
Lys	Asp	Glu	Pro	Thr	Tyr	Ile	Leu	Asn	Ile	Lys	Arg	Gly	Ile	Ile	Ser	115	120	125	
Ala	Leu	Leu	Val	Pro	Pro	Glu	Thr	Glu	Glu	Ala	Lys	Gln	Val	Leu	Phe	130	135	140	
Leu	Asp	Thr	Val	Tyr	Gly	Asn	Cys	Ser	Thr	His	Phe	Thr	Val	Lys	Thr	145	150	155	160
Arg	Lys	Gly	Asn	Val	Ala	Thr	Glu	Ile	Ser	Thr	Glu	Arg	Asp	Leu	Gly	165	170	175	
Gln	Cys	Asp	Arg	Phe	Lys	Pro	Ile	Arg	Thr	Gly	Ile	Ser	Pro	Leu	Ala	180	185	190	
Leu	Ile	Lys	Gly	Met	Thr	Arg	Pro	Leu	Ser	Thr	Leu	Ile	Ser	Ser	Ser	195	200	205	
Gln	Ser	Cys	Gln	Tyr	Thr	Leu	Asp	Ala	Lys	Arg	Lys	His	Val	Ala	Glu	210	215	220	
Ala	Ile	Cys	Lys	Glu	Gln	His	Leu	Phe	Leu	Pro	Phe	Ser	Tyr	Lys	Asn	225	230	235	240
Lys	Tyr	Gly	Met	Val	Ala	Gln	Val	Thr	Gln	Thr	Leu	Lys	Leu	Glu	Asp	245	250	255	

Thr Pro Lys Ile Asn Ser Arg Phe Phe Gly Glu Gly Thr Lys Lys Met  
 260 265 270  
 Gly Leu Ala Phe Glu Ser Thr Lys Ser Thr Ser Pro Pro Lys Gln Ala  
 275 280 285  
 Glu Ala Val Leu Lys Thr Leu Gln Glu Leu Lys Lys Leu Thr Ile Ser  
 290 295 300  
 Glu Gln Asn Ile Gln Arg Ala Asn Leu Phe Asn Lys Leu Val Thr Glu  
 305 310 315 320  
 Leu Arg Gly Leu Ser Asp Glu Ala Val Thr Ser Leu Leu Pro Gln Leu  
 325 330 335  
 Ile Glu Val Ser Ser Pro Ile Thr Leu Gln Ala Leu Val Gln Cys Gly  
 340 345 350  
 Gln Pro Gln Cys Ser Thr His Ile Leu Lys Arg Val His Ala Asn Pro  
 355 360 365  
 Leu Leu Ile Asp Val Val Thr Tyr Leu Val Ala Leu Ile Pro Glu  
 370 375 380

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Phe Gly Leu Ser Asn Lys Ile Asn Ser Lys His Leu Arg Val Asn Gln  
 1 5 10 15  
 Asn Leu Val Tyr Glu Ser Gly Ser Leu Asn Phe Ser Lys Leu Glu Ile  
 20 25 30  
 Gln Ser Gln Val Asp Ser Gln His Val Gly His Ser Val Leu Thr Ala  
 35 40 45  
 Lys Gly Met Ala Leu Phe Gly Glu Gly Lys Ala Glu Phe Thr Gly Arg  
 50 55 60  
 His Asp Ala His Leu Asn Gly Lys Val Ile Gly Thr Leu Lys Asn Ser  
 65 70 75 80  
 Leu Phe Phe Ser Ala Gln Pro Phe Glu Ile Thr Ala Ser Thr Asn Asn  
 85 90 95

Glu Gly Asn Leu Lys Val Arg Phe Pro Leu Arg Leu Thr Gly Lys Ile  
 100 105 110  
 Asp Phe Leu Asn Asn Tyr Ala Leu Phe Leu Ser Pro Ser Ala Gln Gln  
 115 120 125  
 Ala Ser Trp Gln Val Ser Ala Arg Phe Asn Gln Tyr Lys Tyr Asn Gln  
 130 135 140  
 Asn Phe Ser Ala Gly Asn Asn Glu Asn Ile Met Glu Ala His Val Gly  
 145 150 155 160  
 Ile Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn Ile Pro Leu Thr Ile  
 165 170 175  
 Pro Glu Met Arg Leu Pro Tyr Thr Ile Ile Thr Thr Pro Pro Leu Lys  
 180 185 190  
 Asp Phe Ser Leu Trp Glu Lys Thr Gly Leu Lys Glu Phe Leu Lys Thr  
 195 200 205  
 Thr Lys Gln Ser Phe Asp Leu Ser Val Lys Ala Gln Tyr Lys Lys Asn  
 210 215 220  
 Lys His Arg His Ser Ile Asn Pro Leu Ala Val Leu Cys Glu Phe Ile  
 225 230 235 240  
 Ser Gln Ser Ile Lys Ser Phe Asp Arg His Phe Glu Lys Asn Arg Asn  
 245 250 255  
 Asn Ala Leu Asp Phe Val Thr Lys Ser Tyr Asn Glu Thr Lys Ile Lys  
 260 265 270  
 Phe Asp Lys Tyr Lys Ala Glu Lys Ser His Asp Glu Leu Pro Arg Thr  
 275 280 285  
 Phe Gln Ile Pro Gly Tyr Thr Val Pro Val Val Asn Val Glu Val Ser  
 290 295 300  
 Pro Phe Thr Ile Glu Met Ser Ala Phe Gly Tyr Val Phe Pro Lys Ala  
 305 310 315 320  
 Val Ser Met Pro Ser Phe Ser Ile Leu Gly Ser Asp Val Arg Val Pro  
 325 330 335  
 Ser Tyr Thr Leu Ile Leu Pro Ser Leu Glu Leu Pro Val Leu His Val  
 340 345 350  
 Pro Arg Asn Leu Lys Leu Ser Leu Pro His Phe Lys Glu Leu Cys Thr  
 355 360 365  
 Ile Ser His Ile Phe Ile Pro Ala Met Gly Asn Ile Thr Tyr Asp Phe  
 370 375 380

Ser Phe Lys Ser Ser Val Ile Thr Leu Asn  
385 390

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met	Ala	Ser	Gly	Arg	Ala	Arg	Cys	Thr	Arg	Lys	Leu	Arg	Asn	Trp	Val
1				5					10					15	
Val	Glu	Gln	Val	Glu	Ser	Gly	Gln	Phe	Pro	Gly	Val	Cys	Trp	Asp	Asp
			20					25					30		
Thr	Ala	Lys	Thr	Met	Phe	Arg	Ile	Pro	Trp	Lys	His	Ala	Gly	Lys	Gln
			35				40					45			
Asp	Phe	Arg													
			50												

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Pro	Lys	Asp	Ala	Thr	Arg	Phe	Lys	His	Leu	Arg	Lys	Tyr	Thr	Tyr	Asn
1				5					10					15	
Tyr	Glu	Ala	Glu	Ser	Ser	Ser	Gly	Val	Pro	Gly	Thr	Ala	Asp	Ser	Arg
			20					25					30		
Ser	Ala	Thr	Arg	Ile	Asn	Cys	Lys	Val	Glu	Leu	Glu	Val	Leu	Pro	Gln
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

```

Pro Glu Gly Lys Ala Leu Leu Lys Lys Thr Lys Asn Ser Glu Glu Phe
1          5          10          15

Ala Ala Ala Met Ser Arg Tyr Glu Leu Lys Leu Ala Ile Pro Glu Gly
          20          25          30

Lys Gln Val Phe Leu
          35

```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Cys Ser Thr His Phe Thr Val Lys Thr Arg Lys Gly Asn Val Ala Thr  
1 5 10 15  
Glu Ile Ser Thr Glu Arg Asp Leu Gly Gln Cys Asp Arg Phe Lys Pro  
20 25 30  
Ile Arg Thr Gly Ile Ser  
35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

[illegible]

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 38 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

His Leu Ser Cys Asp Thr Lys Glu Glu Arg Lys Ile Lys Gly Val Ile  
1                  5                  10                  15  
  
Ser Ile Pro Arg Leu Gln Ala Glu Ala Arg Ser Glu Ile Leu Ala His  
                  20                  25                  30  
  
Trp Ser Pro Ala Lys Leu  
                  35

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 47 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ser Val His Leu Asp Ser Lys Lys Lys Gln His Leu Phe Val Lys Glu  
1                  5                  10                  15  
  
Val Lys Ile Asp Gly Gln Phe Arg Val Ser Ser Phe Tyr Ala Lys Gly  
                  20                  25                  30  
  
Thr Tyr Gly Leu Ser Cys Gln Arg Asp Pro Asn Thr Gly Arg Leu  
                  35                  40                  45

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Lys His Ile Asn Ile Asp Gln Phe Val Arg Lys Tyr Arg Ala Ala Leu  
1                  5                  10                  15

Gly Lys Leu Pro Gln Gln Ala Asn Asp Tyr Leu Ser Phe Asn Trp Glu  
 20 25 30

Arg Gln Val Ser His Ala Lys Glu  
 35 40

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 40 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Lys Leu Thr Ala Leu Thr Lys Lys Tyr Arg Ile Thr Glu Asn Asp Ile  
 1 5 10 15

Gln Ile Ala Leu Asp Asp Ala Lys Ile Asn Phe Asn Glu Lys Leu Ser  
 20 25 30

Gln Leu Gln Thr Tyr Met Ile Gln  
 35 40

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Glu Arg Ile Asn Asp Val Leu Glu His Val Lys His Phe Val Ile Asn  
 1 5 10 15

Leu Ile Gly Asp Phe Glu Val Ala Glu Lys Ile Asn Ala Phe Arg Ala  
 20 25 30

Lys Val His Glu Leu Ile Glu Arg Tyr Glu Val Asp Gln Gln Ile Gln  
 35 40 45

Val Leu  
 50

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```

Asn Lys Phe Leu Asp Met Leu Ile Lys Lys Leu Lys Ser Phe Asp Tyr
1           5           10           15
His Gln Phe Val Asp Glu Thr Asn Asp Lys Ile Arg Glu Val Thr Gln
          20           25           30
Arg Leu Asn Gly Glu Ile Gln Ala Leu Glu Leu Pro Gln Lys Ala Glu
          35           40           45
Ala Leu
          50

```

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```

Ser Asn Lys Ile Asn Ser Lys His Leu Arg Val Asn Gln Asn Leu Val
1           5           10           15
Tyr Glu Ser Gly Ser Leu Asn
          20

```

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```

Phe Ser Lys Leu Glu Ile Gln Ser Gln Val Asp Ser Gln His Val Gly
1           5           10           15
His Ser Val Leu Thr Ala Lys Gly Met Ala Leu Phe Gly Glu Gly Gly
          20           25           30

```

Lys Ala Glu Phe Thr Gly Arg His Asp Ala His Leu Asn Gly Lys  
 35 40 45

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Val Lys Ala Gln Tyr Lys Lys Asn Lys His Arg His Ser Ile Thr Asn  
 1 5 10 15  
 Pro Leu Ala Val Leu Cys Glu Phe Ile Ser Gln Ser Ile Lys Ser Phe  
 20 25 30  
 Asp Arg His Phe Glu Lys Asn Arg Asn Asn Ala Leu Asp Phe Val Thr  
 35 40 45  
 Lys Ser  
 50

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Lys Leu Glu Gly Thr Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys Leu  
 1 5 10 15  
 Ala Thr Ala Leu Ser Leu Ser Asn Lys Phe Val Glu Gly Ser His Asn  
 20 25 30  
 Ser Thr Val Ser Leu Thr Thr Lys Asn Met Glu Val Ser Val Ala Lys  
 35 40 45  
 Thr Thr Lys  
 50

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids

(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Lys Leu Asp Val Thr Thr Ser Ile Gly Arg Arg Gln His Leu Arg Val  
1 5 10 15  
Ser Thr Ala Phe Val Tyr Thr Lys Asn Pro Asn Gly Tyr Ser Phe Ser  
20 25 30  
Ile Pro Val Lys Val Leu Ala Asp Lys Phe Ile Thr Pro Gly Leu Lys  
35 40 45  
Leu Asn Asp  
50

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Phe Arg Glu Ile Gln Ile Tyr Lys Lys Leu Arg Thr Ser Ser Phe Ala  
1 5 10 15  
Leu Asn Leu Pro Thr Leu Pro Glu Val Lys Phe Pro Glu Val Asp Val  
20 25 30  
Leu Thr Lys Tyr Ser Gln Pro Glu Asp Ser Leu Ile Pro Phe Phe Glu  
35 40 45  
Ile

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Leu His Leu Arg Tyr Gln Lys Asp Lys Lys Gly Ile Ser Thr Ser Ala  
1 5 10 15

Ala Ser Pro Ala Val Gly Thr Val Gly Met Asp Met Asp Glu Asp Asp  
20 25 30

Asp Phe Ser Lys Trp Asn Phe Tyr Tyr Ser Pro Gln Ser Ser Pro Asp  
35 40 45

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Leu Arg Glu Val Ser Ser Lys Leu Arg Arg Asn Leu Gln Asn Asn Ala  
1 5 10 15

Glu Trp Val Tyr Gln Gly Ala Ile Arg Gln Ile Asp Asp Ile Asp Val  
20 25 30

Arg Phe Gln Lys Ala Ala Ser Gly Thr Thr Gly Thr Tyr Gln Glu Trp  
35 40 45

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Arg Val Thr Gln Lys Phe His Met Lys Val Lys His Leu Ile Asp Ser  
1 5 10 15

Leu Ile Asp Phe Leu Asn Phe Pro Arg Phe Gln Phe Pro Gly Lys Pro  
20 25 30

Gly Ile Tyr Thr Arg Glu Glu Leu Cys Thr Met Phe Ile Arg Glu Val  
35 40 45

Gly Thr  
50

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Trp Lys His Ala Gly Lys Gln Asp Phe Arg Glu Ser Gln Asp Ala Ala
1           5           10           15
Ala Phe Phe Lys Ala Trp Ala Ile Phe Lys Gly Lys Tyr Lys Glu Gly
          20           25           30
Asp Lys Glu Val Pro Glu Arg Gly Arg Met Asp Val Ala Glu Pro Tyr
          35           40           45
Lys

```

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 48 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

Glu His Val Lys His Phe Val Ile Asn Leu Ile Gly Asp Phe Glu Val
1           5           10           15
Ala Glu Lys Ile Asn Ala Phe Arg Ala Lys Val His Glu Leu Ile Glu
          20           25           30
Arg Tyr Glu Val Asp Gln Gln Ile Gln Val Leu Met Asp Lys Leu Val
          35           40           45

```

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 52 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```

Val Arg Lys Tyr Arg Ala Ala Leu Gly Lys Leu Pro Gln Gln Ala Asn
1           5           10           15

```

Asp Tyr Leu Asn Ser Phe Asn Trp Glu Arg Gln Val Ser His Ala Lys  
                     20                    25                    30  
 Glu Lys Leu Thr Ala Leu Thr Lys Lys Tyr Arg Ile Thr Glu Asn Asp  
                     35                    40                    45  
 Ile Gln Ile Ala  
                     50

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 57 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Tyr Ile Lys Asp Ser Tyr Asp Leu His Asp Leu Lys Ile Ala Ile Ala  
 1                    5                    10                    15  
 Asn Ile Ile Asp Glu Ile Ile Glu Lys Leu Lys Ser Leu Asp Glu His  
                     20                    25                    30  
 Tyr His Ile Arg Val Asn Leu Val Lys Thr Ile His Asp Leu His Leu  
                     35                    40                    45  
 Phe Ile Glu Asn Ile Asp Phe Asn Lys  
                     50                    55

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 33 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Lys Ile Thr Leu Ile Ile Asn Trp Leu Gln Glu Ala Leu Ser Ser Ala  
 1                    5                    10                    15  
 Ser Leu Ala His Met Lys Ala Lys Phe Arg Glu Thr Leu Glu Asp Thr  
                     20                    25                    30  
 Arg

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Thr	Asp	His	Phe	Ser	Leu	Arg	Ala	Arg	Tyr	His	Met	Lys	Ala	Asp	Ser
1				5					10					15	
Val	Val	Asp	Leu	Ser	Tyr	Asn	Val	Gln	Gly	Ser	Gly	Glu	Thr	Thr	Tyr
			20					25					30		

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Lys	Leu	Thr	Thr	Asn	Gly	Arg	Phe	Arg	Glu	His	Asn	Ala	Lys	Phe	Ser
1				5					10					15	
Leu	Asp	Gly	Lys												
			20												

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Asp	Thr	Lys	Tyr	Gln	Ile	Arg	Ile	Gln	Ile	Gln	Glu	Lys	Leu	Gln	Gln
1				5					10					15	
Leu	Lys	Arg	His	Ile	Gln	Asn	Ile	Asp	Ile	Gln	His	Leu	Ala	Gly	Lys
			20					25					30		
Leu	Lys	Gln	His	Ile	Glu	Ala	Ile	Asp	Val	Arg	Val	Leu	Leu	Asp	Gln
		35					40					45			

Leu Gly Thr Thr  
50

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe	His	Asp	Phe	Pro	Asp	Leu	Gly	Gln	Glu	Val	Ala	Leu	Asn	Ala	Asn
1				5					10					15	
Thr	Lys	Asn	Gln	Lys	Ile	Arg	Trp	Lys	Asn	Glu	Val	Arg	Ile	His	Ser
			20					25					30		
Gly	Ser	Phe	Gln	Ser	Gln	Val	Glu	Leu	Ser	Asn	Asp	Gln			
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Lys	Asp	Asn	Val	Phe	Asp	Gly	Leu	Val	Arg	Val	Thr	Gln	Lys	Phe	His
1				5					10					15	
Met	Lys	Val	Lys	His	Leu	Ile	Asp	Ser	Leu	Ile	Asp	Phe	Leu	Asn	Phe
			20					25					30		
Pro	Arg														

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

His	Arg	Asn	Ile	Gln	Glu	Tyr	Leu	Ser	Ile	Leu	Thr	Asp	Pro	Asp	Gly
1				5					10					15	
Lys	Gly	Lys	Glu	Lys	Ile	Ala	Glu	Leu	Ser	Ala	Thr	Ala	Gln	Glu	Ile
			20					25					30		
Ile	Lys	Ser													

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Glu	Phe	Thr	Ile	Val	Ala	Phe	Val	Lys	Tyr	Asp	Lys	Asn	Gln	Asp	Val
1				5				10					15		
His	Ser	Ile	Asn	Leu	Pro	Phe	Phe	Glu	Thr	Leu	Gln	Glu	Tyr	Phe	Glu
			20					25					30		
Arg	Asn	Arg	Gln	Thr	Ile	Val	Val	Val	Glu	Asn	Val	Gln	Arg	Asn	Leu
		35					40					45			
Lys	His	Ile	Asn	Ile	Asp	Gln	Phe	Val	Arg	Lys	Tyr	Arg	Ala	Ala	Leu
	50					55					60				
Gly	Lys	Leu	Pro	Gln	Gln	Ala	Asn	Asp	Tyr	Leu	Asn	Ser	Phe	Asn	Trp
65				70						75				80	
Glu	Arg	Gln	Val	Ser	His	Ala	Lys	Glu	Lys	Leu	Thr	Ala	Leu	Thr	Lys
				85					90					95	
Lys	Tyr	Arg	Ile	Thr	Glu	Asn	Asp	Ile	Gln	Ile	Ala	Leu	Asp	Asp	Ala
			100					105					110		
Lys	Ile	Asn	Phe	Asn	Glu	Lys	Leu	Ser	Gln	Leu	Gln	Thr	Tyr	Met	Ile
		115					120					125			
Gln	Phe	Asp	Gln	Tyr	Ile	Lys	Asp	Ser	Tyr	Asp	Leu	His	Asp	Leu	Lys
		130				135					140				
Ile	Ala	Ile	Ala	Asn	Ile	Ile	Asp	Glu	Ile	Ile	Glu	Lys	Leu	Lys	Ser
145					150					155				160	
Leu	Asp	Glu	His	Tyr	His	Ile	Arg	Val	Asn	Leu	Val	Lys	Thr	Ile	His
				165					170					175	

Asp Leu His Leu Phe Ile Glu Asn Ile Asp Phe Asn Lys Ser Gly Ser  
180 185 190

Ser Thr Ala Ser Trp Ile Gln Asn Val Asp Thr Lys Tyr Gln Ile Arg  
195 200 205

Ile Gln  
210

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Gly Pro Leu Pro Thr Leu Val Ser Gly Gly Thr Ile Leu Ala Thr Val  
1 5 10 15

Pro Leu Val Val Asp Ala Glu Lys Leu Pro Ile Asn Arg Leu Ala Ala  
20 25 30

Gly Ser Lys Ala Pro Ala Ser Ala Gln Ser Arg Gly Glu Lys Arg Thr  
35 40 45

Ala His Asn Ala Ile Glu Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys  
50 55 60

Ile Ile Glu Leu Lys Asp Leu Val Val Gly Thr Glu Ala Lys Leu Asn  
65 70 75 80

Lys Ser Ala Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg Phe Leu Gln  
85 90 95

His Ser Asn Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu Arg Thr Ala  
100 105 110

Val His Lys Ser Lys Ser Leu Lys Asp Leu Val Ser Ala Cys Gly Ser  
115 120 125

Gly Gly Asn Thr Asp Val Leu Met Glu Gly Val Lys Thr Glu Val Glu  
130 135 140

Asp Thr Leu Thr Pro Pro Pro Ser Asp Ala Gly Ser Pro Phe Gln Ser  
145 150 155 160

Ser Pro Leu Ser Leu Gly Ser Arg Gly Ser Gly Ser Gly Gly  
165 170

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Gln Val Pro Thr Leu Val Gly Ser Ser Gly Thr Ile Leu Thr Thr Met  
1                      5                      10                      15

Pro Val Met Met Gly Gln Glu Lys Val Pro Ile Lys Gln Val Pro Gly  
                    20                      25                      30

Gly Val Lys Gln Leu Glu Pro Pro Lys Glu Gly Glu Arg Arg Thr Thr  
                    35                      40                      45

His Asn Ile Ile Glu Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys Ile  
50                      55                      60

Ile Glu Leu Lys Asp Leu Val Met Gly Thr Asp Ala Lys Met His Lys  
65                      70                      75                      80

Ser Gly Val Leu Arg Lys Ala Ile Asp Tyr Ile Lys Tyr Leu Gln Gln  
                    85                      90                      95

Val Asn His Lys Leu Arg Gln Glu Asn Met Val Leu Lys Leu Ala Asn  
                    100                      105                      110

Gln Lys Asn Lys Leu Leu Lys Gly Ile Asp Leu Gly Ser Leu Val Asp  
                    115                      120                      125

Asn Glu Val Asp Leu Lys Ile Glu Asp Phe Asn Gln Asn Val Leu Leu  
130                      135                      140

Met Ser Pro Pro Ala Ser Asp Ser Gly Ser Gln Ala Gly Phe Ser Pro  
145                      150                      155                      160

Tyr Ser Ile Asp Ser Glu Pro Gly Ser Pro Leu Leu  
                    165                      170

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Gly Pro Leu Gln Thr Leu Val Ser Gly Gly Thr Ile Leu Ala Thr Val  
1 5 10 15  
Pro Leu Val Val Asp Thr Asp Lys Leu Pro Ile His Arg Leu Ala Ala  
20 25 30  
Gly Gly Lys Ala Leu Gly Ser Ala Gln Ser Arg Gly Glu Lys Arg Thr  
35 40 45  
Ala His Asn Ala Ile Glu Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys  
50 55 60  
Ile Val Glu Leu Lys Asp Leu Val Val Gly Thr Glu Ala Lys Leu Asn  
65 70 75 80  
Lys Ser Ala Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg Phe Leu Gln  
85 90 95  
His Ser Asn Gln Lys Leu Lys Gln Glu Asn Leu Thr Leu Arg Ser Ala  
100 105 110  
His Lys Ser Lys Ser Leu Lys Asp Leu Val Ser Ala Cys Gly Ser Gly  
115 120 125  
Gly Gly Thr Asp Val Ser Met Glu Gly Met Lys Pro Glu Val Val Glu  
130 135 140  
Thr Leu Thr Pro Pro Pro Ser Asp Ala Gly Ser Pro Ser Gln Ser Ser  
145 150 155 160  
Pro Leu Ser Leu Gly Ser Arg Gly Ser Ser Ser Gly Gly  
165 170

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 243 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Asp Glu Pro Pro Gln Ser Pro Trp Asp Arg Val Lys Asp Leu Ala Thr  
1 5 10 15  
Val Tyr Val Asp Val Leu Lys Asp Ser Gly Arg Asp Tyr Val Ser Gln  
20 25 30  
Phe Glu Gly Ser Ala Leu Gly Lys Gln Leu Asn Leu Lys Leu Leu Asp  
35 40 45

Asn Trp Asp Ser Val Thr Ser Thr Phe Ser Lys Leu Arg Glu Gln Leu  
 50 55 60  
 Gly Pro Val Thr Gln Glu Phe Trp Asp Asn Leu Glu Lys Glu Thr Glu  
 65 70 75 80  
 Gly Leu Arg Gln Glu Met Ser Lys Asp Leu Glu Glu Val Lys Ala Lys  
 85 90 95  
 Val Gln Pro Tyr Leu Asp Asp Phe Gln Lys Lys Trp Gln Glu Glu Met  
 100 105 110  
 Glu Leu Tyr Arg Gln Lys Val Glu Pro Leu Arg Ala Glu Leu Gln Glu  
 115 120 125  
 Gly Ala Arg Gln Lys Leu His Glu Leu Gln Glu Lys Leu Ser Pro Leu  
 130 135 140  
 Gly Glu Glu Met Arg Asp Arg Ala Arg Ala His Val Asp Ala Leu Arg  
 145 150 155 160  
 Thr His Leu Ala Pro Tyr Ser Asp Glu Leu Arg Gln Arg Leu Ala Ala  
 165 170 175  
 Arg Leu Glu Ala Leu Lys Glu Asn Gly Gly Ala Arg Leu Ala Glu Tyr  
 180 185 190  
 His Ala Lys Ala Thr Glu His Leu Ser Thr Leu Ser Glu Lys Ala Lys  
 195 200 205  
 Pro Ala Leu Glu Asp Leu Arg Gln Gly Leu Leu Pro Val Leu Glu Ser  
 210 215 220  
 Phe Lys Val Ser Phe Leu Ser Ala Leu Glu Glu Tyr Thr Lys Lys Leu  
 225 230 235 240  
 Asn Thr Gln

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Gln Gln Val Pro Val Leu Leu Gln Pro His Phe Ile Lys Ala Asp Ser  
 1 5 10 15

Leu Leu Leu Thr Ala Met Lys Thr Asp Gly Ala Thr Val Lys Ala Ala  
 20 25 30  
 Gly Leu Ser Pro Leu Val Ser Gly Thr Thr Val Gln Thr Gly Pro Leu  
 35 40 45  
 Pro Thr Leu Val Ser Gly Gly Thr Ile Leu Ala Thr Val Pro Leu Val  
 50 55 60  
 Val Asp Ala Glu Lys Leu Pro Ile Asn Arg Leu Ala Ala Gly Ser Lys  
 65 70 75 80  
 Ala Pro Ala Ser Ala Gln Ser Arg Gly Glu Lys Arg Thr Ala His Asn  
 85 90 95  
 Ala Ile Glu Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys Ile Ile Glu  
 100 105 110  
 Leu Lys Asp Leu Val Val Gly Thr Glu Ala Lys Leu Asn Lys Ser Ala  
 115 120 125  
 Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg Phe Leu Gln His Ser Asn  
 130 135 140  
 Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu Arg Thr Ala Val His Lys  
 145 150 155 160  
 Ser Lys Ser Leu Lys Asp Leu Val Ser Ala Cys Gly Ser Gly Gly Asn  
 165 170 175  
 Thr Asp Val Leu Met Glu Gly Val Lys Thr Glu Val Glu Asp Thr Leu  
 180 185 190  
 Thr Pro Pro Pro Ser Asp Ala Gly Ser Pro Phe Gln Ser Ser Pro Leu  
 195 200 205  
 Ser Leu Gly Ser Arg Gly Ser Gly Ser Gly Gly Ser Gly Ser Asp Ser  
 210 215 220  
 Glu Pro Asp Ser Pro Val Phe Glu Asp Ser Lys Ala Lys Pro Glu Gln  
 225 230 235 240  
 Arg Pro Ser Leu His Ser Arg Gly Met Leu Asp Arg Ser Arg Leu Leu  
 245 250 255  
 Ala Leu Cys Thr Leu Val Phe Leu Cys Leu Ser Cys Asn  
 260 265

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 amino acids
  - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Gln	Ala	Lys	Glu	Pro	Cys	Val	Glu	Ser	Leu	Val	Ser	Gln	Tyr	Phe	Gln
1				5					10					15	
Thr	Val	Thr	Asp	Tyr	Gly	Lys	Asp	Leu	Met	Glu	Lys	Val	Lys	Ser	Pro
			20					25					30		
Glu	Leu	Gln	Ala	Glu	Ala	Lys	Ser	Tyr	Phe	Glu	Lys	Ser	Lys	Glu	Gln
		35					40					45			
Leu	Thr	Pro	Leu	Ile	Lys	Lys	Ala	Gly	Thr	Glu	Leu	Val	Asn	Phe	Leu
	50					55						60			
Ser	Tyr	Phe	Val	Glu	Leu	Gly	Thr	Gln	Pro	Ala	Thr	Gln			
65					70					75					

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 71 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Glu	Ala	Lys	Leu	Asn	Lys	Ser	Ala	Val	Leu	Arg	Lys	Ala	Ile	Asp	Tyr
1				5					10					15	
Ile	Arg	Phe	Leu	Gln	His	Ser	Asn	Gln	Lys	Leu	Lys	Gln	Glu	Asn	Leu
			20					25					30		
Ser	Leu	Arg	Thr	Ala	Val	His	Lys	Ser	Lys	Ser	Leu	Lys	Asp	Leu	Val
		35					40					45			
Ser	Ala	Cys	Gly	Ser	Gly	Gly	Asn	Thr	Asp	Val	Leu	Met	Glu	Gly	Val
	50					55					60				
Lys	Thr	Glu	Val	Glu	Asp	Thr									
65					70										

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 397 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gln	Lys	Ser	Glu	Leu	Thr	Gln	Gln	Leu	Asn	Ala	Leu	Phe	Gln	Asp	Lys	
1				5					10					15		
Leu	Gly	Glu	Val	Asn	Thr	Tyr	Ala	Gly	Asp	Leu	Gln	Lys	Lys	Leu	Val	
			20					25					30			
Pro	Phe	Ala	Thr	Glu	Leu	His	Glu	Arg	Leu	Ala	Lys	Asp	Ser	Glu	Lys	
		35					40					45				
Leu	Lys	Glu	Glu	Ile	Gly	Lys	Glu	Leu	Glu	Glu	Leu	Arg	Ala	Arg	Leu	
	50					55					60					
Leu	Pro	His	Ala	Asn	Glu	Val	Ser	Gln	Lys	Ile	Gly	Asp	Asn	Leu	Arg	
65						70				75					80	
Glu	Leu	Gln	Gln	Arg	Leu	Glu	Pro	Tyr	Ala	Asp	Gln	Leu	Arg	Thr	Gln	
				85					90					95		
Val	Asn	Thr	Gln	Ala	Glu	Gln	Leu	Arg	Arg	Gln	Leu	Asp	Pro	Leu	Ala	
			100					105					110			
Gln	Arg	Met	Glu	Arg	Val	Leu	Arg	Glu	Asn	Ala	Asp	Ser	Leu	Gln	Ala	
		115					120					125				
Ser	Leu	Arg	Pro	His	Ala	Asp	Glu	Leu	Lys	Ala	Lys	Ile	Asp	Gln	Asn	
	130					135					140					
Val	Glu	Glu	Leu	Lys	Gly	Arg	Leu	Thr	Pro	Tyr	Ala	Asp	Glu	Phe	Lys	
145					150					155					160	
Val	Lys	Ile	Asp	Gln	Thr	Val	Glu	Glu	Leu	Arg	Arg	Ser	Leu	Ala	Pro	
				165					170					175		
Tyr	Ala	Gln	Asp	Thr	Gln	Glu	Lys	Leu	Asn	His	Gln	Leu	Glu	Gly	Leu	
			180					185					190			
Thr	Phe	Gln	Met	Lys	Lys	Asn	Ala	Glu	Glu	Leu	Lys	Ala	Arg	Ile	Ser	
		195					200					205				
Ala	Ser	Ala	Glu	Ile	Asp	Gln	Thr	Val	Glu	Glu	Leu	Arg	Arg	Ser	Leu	
		210				215					220					
Ala	Pro	Tyr	Ala	Gln	Asp	Thr	Gln	Glu	Lys	Leu	Asn	His	Gln	Leu	Glu	
225					230					235					240	
Gly	Leu	Thr	Phe	Gln	Met	Lys	Lys	Asn	Ala	Glu	Glu	Leu	Lys	Ala	Arg	
				245				250						255		
Ile	Ser	Ala	Ser	Ala	Glu	Glu	Leu	Arg	Gln	Arg	Leu	Ala	Pro	Leu	Ala	
			260					265					270			



Glu Asp Val Arg Gly Asn Leu Lys Gly Asn Thr Glu Gly Leu Gln Lys  
 275 280 285  
 Ser Leu Ala Glu Leu Gly Gly His Leu Asp Gln Gln Val Glu Glu Phe  
 290 295 300  
 Arg Arg Arg Val Glu Pro Tyr Gly Glu Asn Phe Asn Lys Ala Leu Val  
 305 310 315 320  
 Gln Gln Met Glu Gln Leu Arg Gln Lys Leu Gly Pro His Ala Gly Asp  
 325 330 335  
 Val Glu Gly His Leu Ser Phe Leu Glu Lys Asp Leu Arg Asp Lys Val  
 340 345 350  
 Asn Ser Phe Phe Ser Thr Phe Lys Glu Lys Glu Ser Gln Asp Lys Thr  
 355 360 365  
 Leu Ser Leu Pro Glu Leu Glu Gln Gln Gln Glu Gln Gln Glu Gln  
 370 375 380  
 Gln Gln Glu Gln Val Gln Met Leu Ala Pro Leu Glu Ser  
 385 390 395

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 412 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Glu Lys Leu Pro Ile Asn Arg Leu Ala Ala Gly Ser Lys Ala Pro Ala  
 1 5 10 15  
 Ser Ala Gln Ser Arg Gly Glu Lys Arg Thr Ala His Asn Ala Ile Glu  
 20 25 30  
 Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys Ile Ile Glu Leu Lys Asp  
 35 40 45  
 Leu Val Val Gly Thr Glu Ala Lys Leu Asn Lys Ser Ala Val Leu Arg  
 50 55 60  
 Lys Ala Ile Asp Tyr Ile Arg Phe Leu Gln His Ser Asn Gln Lys Leu  
 65 70 75 80  
 Lys Gln Glu Asn Leu Ser Leu Arg Thr Ala Val His Lys Ser Lys Ser  
 85 90 95

Leu Lys Asp Leu Val Ser Ala Cys Gly Ser Gly Gly Asn Thr Asp Val  
 100 105 110

Leu Met Glu Gly Val Lys Thr Glu Val Glu Asp Thr Leu Thr Pro Pro  
 115 120 125

Pro Ser Asp Ala Lys Pro Phe Gln Ser Ser Pro Leu Ser Leu Lys Arg  
 130 135 140

Lys Lys Gly Lys Lys Asp Ser Glu Pro Asp Ser Pro Val Phe Glu Asp  
 145 150 155 160

Ser Lys Ala Lys Pro Glu Gln Arg Pro Ser Leu His Ser Arg Gly Met  
 165 170 175

Leu Asp Arg Ser Arg Leu Ala Leu Cys Thr Leu Val Phe Leu Cys Leu  
 180 185 190

Ser Cys Asn Pro Leu Ala Ser Leu Leu Gly Ala Arg Gly Leu Pro Ser  
 195 200 205

Pro Ser Asp Thr Thr Ser Val Tyr His Ser Pro Gly Arg Asn Val Leu  
 210 215 220

Gly Thr Glu Arg Asp Gly Pro Gly Trp Ala Gln Ala Val Gln Leu Phe  
 225 230 235 240

Leu Cys Asp Leu Leu Leu Val Ala Thr Ser Leu Trp Arg Gln Gln Gln  
 245 250 255

Pro Pro Ala Pro Ala Pro Ala Ala Gln Gly Ala Ser Ser Arg Pro Gln  
 260 265 270

Ala Ser Ala Leu Glu Ile Arg Gly Phe Gln Arg Asp Leu Ser Ser Leu  
 275 280 285

Arg Arg Leu Ala Gln Ser Phe Arg Pro Ala Met Arg Arg Val Phe Leu  
 290 295 300

His Glu Ala Thr Ala Arg Leu Met Ala Gly Ala Ser Pro Thr Arg Thr  
 305 310 315 320

His Gln Leu Leu Asp Arg Ser Leu Arg Arg Arg Ala Gly Pro Gly Gly  
 325 330 335

Lys Gly Gly Ala Ala Glu Leu Glu Pro Arg Pro Thr Arg Arg Glu His  
 340 345 350

Ala Glu Ala Leu Leu Leu Ala Ser Cys Tyr Leu Pro Pro Gly Phe Leu  
 355 360 365

Ser Ala Pro Gly Gln Arg Val Gly Met Leu Ala Glu Ala Arg Thr Leu  
 370 375 380

Glu Lys Leu Gly Asp Arg Arg Leu Leu His Asp Cys Gln Gln Met Leu  
 385 390 395 400

Met Arg Leu Gly Gly Gly Thr Thr Val Thr Ser Ser  
 405 410

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Glu Lys Met Ser Leu Arg Asn Arg Leu Ser Lys Ser Arg Glu Asn Pro  
 1 5 10 15

Glu Glu Asp Glu Asp Gln Arg Asn Pro Ala Lys Glu Ser Leu Glu Thr  
 20 25 30

Pro Ser Asn Gly Arg Ile Asp Ile Lys Gln Leu Ile Ala Lys Lys Ile  
 35 40 45

Lys Leu Thr Ala Glu Asn Gly Arg Ile Asp Ile Lys Gln Leu Ile Ala  
 50 55 60

Lys Lys Ile Lys Leu Thr Ala Glu Ala Glu Glu Leu Lys Pro Phe Phe  
 65 70 75 80

Met Lys Glu Val Gly Ser His Phe Asp Asp Phe Val Thr Asn Leu Ile  
 85 90 95

Glu Lys Ser Ala Ser Leu Asp Asn Lys Ala His Ser Phe Val Arg Glu  
 100 105 110

Asn Val Pro Arg Val Leu Asn Ser Ala Lys Glu Lys  
 115 120

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Glu Lys Leu Pro Ile Asn Arg Leu Ala Ala Gly Ser Lys Ala Pro Ala  
 1 5 10 15

Ser Ala Gln Ser Arg Gly Glu Lys Arg Thr Ala His Asn Ala Ile Glu  
 20 25 30  
 Lys Arg Tyr Arg Ser Ser Ile Asn Asp Lys Ile Ile Glu Leu Lys Asp  
 35 40 45  
 Leu Val Val Gly Thr Glu Ala Lys Leu Asn Lys Ser Tyr Ile Arg Phe  
 50 55 60  
 Leu Gln His Ser Asn Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu Arg  
 65 70 75 80  
 Thr Ala Val His Lys Ser Lys Ser Leu Lys Asp Leu Val Ser Ala Cys  
 85 90 95  
 Gly Ser Gly Gly Asn Thr Asp Val Leu Met Glu Gly Val Lys Thr Glu  
 100 105 110  
 Val Glu Asp Lys Ala Lys Pro Glu Gln Arg Pro Ser Leu His Ser Arg  
 115 120 125  
 Gly Met Leu Asp Arg Ser Arg  
 130 135

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Arg Arg His Cys Pro Leu Lys Asn Pro Thr Phe Leu Asp Tyr Val Arg  
 1 5 10 15  
 Pro Arg Ser Trp Thr Cys Arg Tyr Val Phe  
 20 25

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Ser	Gln	Ile	Gln	Gln	Val	Pro	Val	Leu	Leu	Gln	Pro	His	Phe	Ile	Lys
1				5					10					15	
Ala	Asp	Ser	Leu	Leu	Leu	Thr	Ala	Met	Lys	Thr	Asp	Gly	Ala	Thr	Val
			20					25					30		
Lys	Ala	Ala	Gly	Leu	Ser	Pro	Leu	Val	Ser	Gly	Thr	Thr			
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Ser	Leu	Leu	Ser	Phe	Met	Gln	Gly	Tyr	Met	Lys	His	Ala	Thr	Lys	Thr
1				5					10					15	
Ala	Lys	Asp	Ala	Leu	Ser	Ser	Val	Gln	Glu	Ser	Gln	Val	Ala	Gln	Gln
			20					25					30		
Ala	Arg	Gly	Trp	Val	Thr	Asp	Gly	Phe	Ser	Ser	Leu	Lys			
		35					40					45			

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Ala	Pro	Ala	Ser	Ala	Gln	Ser	Arg	Gly	Glu	Lys	Arg	Thr	Ala	His	Asn
1				5					10					15	
Ala	Ile	Glu	Lys	Arg	Tyr	Arg	Ser	Ser	Ile	Asn	Asp	Lys	Ile	Ile	Glu
			20					25					30		
Leu	Lys	Asp	Leu	Val	Val	Gly	Thr	Glu	Ala	Lys	Leu	Asn	Lys	Ser	
			35				40					45			

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Asp Tyr Trp Ser Thr Val Lys Asp Lys Phe Ser Glu Phe Trp Asp Leu  
1                   5                   10                   15

Asp Pro Glu Val Arg Pro Thr Ser Ala Val Ala Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Glu Ile Tyr Val Ala Ala Ala Leu Arg Val Lys Thr Ser Leu Pro Arg  
1 5 10 15

Ala Leu His Phe Leu Thr Arg Phe Phe Leu Ser Ser Ala Arg Gln Ala  
20 25 30

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Glu Lys Ile Pro Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Glu Lys Leu Pro Ile  
1 5

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Glu Asn Gly Arg Cys Ile Gln Ala Asn Tyr Ser Leu Met Glu Asn Gly  
1 5 10 15  
Lys Ile Lys Val Leu Asn Gln Glu Leu Arg Ala Asp Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ala Val Leu Arg Lys Ala Ile Asp Tyr Ile Arg Phe Leu Gln His Ser  
1 5 10 15  
Asn Gln Lys Leu Lys Gln Glu Asn Leu Ser Leu Arg Thr Ala Val  
20 25 30

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Met Lys Gln Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr  
1 5 10 15

His Leu Glu Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Lys His Glu Ile Gln Glu Met Phe Asp Gln Leu Arg Ala Lys Glu Lys  
 1 5 10 15  
 Glu Leu Arg Thr Trp Glu Glu Glu Leu Thr Arg Ala Ala Leu Gln Gln  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:143:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Glu Glu Leu Leu Arg Arg Arg Glu Gln Glu Leu Ala Glu Arg Glu Ile  
 1 5 10 15  
 Asp Ile Leu Glu Arg Glu Leu Asn Ile Ile Ile His Gln Leu Cys Gln  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Arg Ile Gln Ile Gln Glu Lys Leu Gln Gln Leu Lys Arg His Ile Gln  
 1 5 10 15  
 Asn Ile Asp Ile Gln His Leu Ala Gly Lys Leu Lys Gln His Ile Glu  
 20 25 30



- (A) LENGTH: 35 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

[illegible]

(2) INFORMATION FOR SEQ ID NO:146:

- (A) LENGTH: 31 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Glu Leu Ser Phe Lys Thr Phe Ile Glu Asp Val Asn Lys Phe Leu Asp  
 1 5 10 15  
 Met Leu Ile Lys Lys Leu Lys Ser Phe Asp Tyr His Gln Phe Val  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:147:

- (A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

His Gln Phe Val Asp Glu Thr Asn Asp Lys Ile Arg Glu Val Thr Gln  
1 5 10 15  
Arg Leu Asn Gly Glu Ile Gln Ala Leu Glu Leu Pro  
20 25

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 31 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Ala Ala Lys Asn Leu Thr Asp Phe Ala Glu Gln Tyr Ser Ile Gln Asp  
1                    5                    10                    15  
Trp Ala Lys Arg Met Lys Ala Leu Val Glu Gln Gly Phe Thr Val  
                    20                    25                    30

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Ser Ala Ser Leu Ala His Met Lys Ala Lys Phe Arg Glu Thr Leu Glu  
1                    5                    10                    15  
Asp Thr Arg Asp Arg Met Tyr Asp Met Asp Ile Gln Gln Glu Leu Gln  
                    20                    25                    30  
Arg Tyr Leu  
                    35

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 35 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Cys Leu Asn Leu His Lys Phe Asn Glu Phe Ile Gln Asn Glu Leu Gln  
1                    5                    10                    15  
Glu Ala Ser Gln Glu Leu Gln Gln Ile His Gln Tyr Ile Met Ala Leu  
                    20                    25                    30

Arg Glu Glu  
35

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Phe Leu Ile Tyr Ile Thr Glu Leu Leu Lys Lys Leu Gln Ser Thr Thr  
1                      5                      10                      15

Val Met Asn Pro Tyr Met Lys Leu Ala Pro Gly Glu Leu Thr Ile Ile  
                    20                      25                      30

Leu

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Arg Leu Leu Asp His Arg Val Pro Glu Thr Asp Met Thr Phe Arg His  
1                      5                      10                      15

Val Gly Ser Lys Leu Ile Val Ala Met Ser Ser Trp Leu Gln  
                    20                      25                      30

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Leu Asn Phe Ser Lys Leu Glu Ile Gln Ser Gln Val Asp Ser Gln His  
1                      5                      10                      15

Val Gly His Ser Val Leu Thr Ala Lys Gly Met Ala Leu Phe  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Asn Gln Asn Phe Ser Ala Gly Asn Asn Glu Asn Ile Met Glu Ala His  
 1 5 10 15

Val Gly Ile Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn Ile  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Met Val Val Thr Arg Ile Ala Pro Ser Pro Thr Gly Asp Pro His Val  
 1 5 10 15

Gly Thr Ala Tyr Ile Ala Leu Phe Asn Tyr Ala Trp Ala  
 20 25

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Thr Thr Val His Thr Arg Phe Pro Pro Glu Pro Asn Gly Tyr Leu His  
 1 5 10 15

Ile Gly His Ala Lys Ser Ile Cys Leu Asn Phe Gly Ile Ala  
 20 25 30

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Lys Ile Lys Leu Tyr Cys Gly Val Asp Pro Thr Ala Gln Ser Leu His  
1                      5                      10                      15  
  
Leu Gly Asn Leu Val Pro Met Val Leu Leu His Phe Tyr Val  
                    20                      25                      30

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Pro Ile Ala Leu Tyr Cys Gly Phe Asp Pro Thr Ala Asp Ser Leu His  
1                      5                      10                      15  
  
Leu Gly His Leu Val Pro Leu Leu Cys Leu Lys Arg Gly Gln  
                    20                      25                      30

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Arg Val Thr Leu Tyr Cys Gly Phe Asp Pro Thr Ala Asp Ser Leu His  
1                      5                      10                      15  
  
Ile Gly Asn Leu Ala Ala Ile Leu Thr Leu Arg Arg Phe Gln  
                    20                      25                      30

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Arg Ile Gly Ala Tyr Val Gly Ile Asp Pro Thr Ala Pro Ser Leu His  
1                      5                      10                      15  
Val Gly His Leu Leu Pro Leu Met Pro Leu Phe Trp Met Tyr  
                    20                      25                      30

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Pro Ile Ala Leu Tyr Cys Gly Phe Asp Pro Thr Ala Asp Ser Leu His  
1                      5                      10                      15  
Leu Gly His Leu Val Pro Leu Leu Cys Leu Lys Arg Phe Gln  
                    20                      25                      30

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Pro Leu Lys Val Lys Leu Gly Ala Asp Pro Thr Ala Pro Asp Ile His  
1                      5                      10                      15  
Ile Gly His His Thr Val Val Leu Asn Lys Leu Arg Gln Phe Gln  
                    20                      25                      30

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Val	Ser	Lys	Gly	Leu	Leu	Ile	Phe	Asp	Ala	Ser	Ser	Ser	Met	Gly	Pro
1				5					10					15	
Gln	Met	Ser	Ala	Ser	Val	His	Leu	Asp	Ser	Lys	Lys	Lys	Gln	His	Leu
			20					25					30		
Phe	Val	Lys	Glu	Val	Lys	Ile	Asp	Gly	Gln	Phe					
			35				40								

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Thr	Ile	Ile	Thr	Thr	Pro	Pro	Leu	Lys	Asp	Phe	Ser	Leu	Trp	Glu	Lys
1				5					10					15	
Thr	Gly	Leu	Lys	Glu	Phe	Leu	Lys	Thr	Thr	Lys	Gln	Ser	Phe	Asp	Leu
			20					25					30		
Ser	Val	Lys	Ala	Gln	Tyr	Lys	Lys	Asn	Lys	His					
			35				40								

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Lys	Asn	Arg	Asn	Asn	Ala	Leu	Asp	Phe	Val	Thr	Lys	Ser	Tyr	Asn	Glu
1				5					10					15	

Thr Lys Ile Lys Phe Asp Lys Tyr Lys Ala Glu Lys Ser Gln Asp Glu  
 20 25 30

Leu Pro Arg Thr Phe Gln Ile  
 35

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Asp Ala Leu Gln Tyr Lys Leu Glu Gly Thr Thr Arg Leu Thr Arg Lys  
 1 5 10 15

Arg Gly Leu Lys Leu Ala Thr Ala Leu Ser Leu Ser Asn Lys Phe Val  
 20 25 30

Glu Gly Ser His  
 35

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Arg Ala Phe Gly Trp Glu Ala Pro Arg Phe Tyr His Met Pro Leu Leu  
 1 5 10 15

Arg Asn Pro Asp Lys Thr Lys Ile Ser Lys Arg Lys Ser His Thr Ser  
 20 25 30

Leu Asp Trp Tyr Lys Ala Glu Gly Phe Leu  
 35 40

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



Asp	Asn	Ile	Thr	Ile	Pro	Val	His	Pro	Arg	Gln	Tyr	Glu	Phe	Ser	Arg
1				5					10					15	
Leu	Asn	Leu	Glu	Tyr	Thr	Val	Met	Ser	Lys	Arg	Lys	Leu	Asn	Leu	Leu
			20					25					30		
Val	Thr	Asp	Lys	His	Val	Glu	Gly	Trp	Asp						
		35					40								

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Lys	Asn	Lys	Gly	Leu	Pro	Phe	Gly	Ile	Thr	Val	Pro	Leu	Leu	Thr	Thr
1				5					10					15	
Ala	Thr	Gly	Glu	Lys	Phe	Gly	Lys	Ser	Ala	Gly	Asn	Ala	Val	Phe	Ile
			20					25					30		
Asp	Pro	Ser	Ile	Asn	Thr	Ala	Tyr								
		35					40								

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 41 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

Arg	Leu	His	Gln	Asn	Gln	Val	Phe	Gly	Leu	Thr	Val	Pro	Leu	Ile	Thr
1				5					10					15	
Lys	Ala	Asp	Gly	Thr	Lys	Phe	Gly	Lys	Thr	Glu	Gly	Gly	Ala	Val	Trp
			20					25					30		
Leu	Asp	Pro	Lys	Lys	Thr	Ser	Pro	Tyr							
		35					40								

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Lys Thr Lys Gly Glu Ala Arg Ala Phe Gly Leu Thr Ile Pro Leu Val  
1                      5                      10                      15  
Thr Lys Ala Asp Gly Thr Lys Phe Gly Lys Thr Glu Ser Gly Thr Ile  
                    20                      25                      30  
Trp Leu Asp Lys Glu Lys Thr Ser Pro Tyr  
                    35                      40

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Lys Thr Ala Leu Asp Glu Cys Val Gly Phe Thr Val Pro Leu Leu Thr  
1                      5                      10                      15  
Asp Ser Ser Gly Ala Lys Phe Gly Lys Ser Ala Gly Asn Ala Ile Trp  
                    20                      25                      30  
Leu Asp Pro Tyr Gln Thr Ser Val Phe  
                    35                      40

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Arg Leu His Gln Asn Gln Val Phe Gly Leu Thr Val Pro Leu Ile Thr  
1                      5                      10                      15

Lys Ala Asp Gly Thr Lys Phe Gly Lys Thr Glu Gly Gly Ala Val Trp  
 20 25 30

Leu Asp Pro Lys Lys Thr Ser Pro Tyr  
 35 40

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Ser Ala Gly Lys Lys Pro Gln Val Ala Ile Thr Leu Pro Leu Leu Val  
 1 5 10 15

Gly Leu Asp Gly Glu Lys Lys Met Ser Lys Ser Leu Gly Asn Tyr Ile  
 20 25 30

Gly Val Thr Glu Ala Pro Ser Asp Met Phe  
 35 40

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Arg Val Ser Thr Ala Phe Val Tyr Thr Lys Asn Pro Asn Gly Tyr Ser  
 1 5 10 15

Phe Ser Ile Pro Val Lys Val Leu Ala Asp Lys Phe Ile Thr Pro Gly  
 20 25 30

Leu Lys Leu  
 35

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr Trp Asn  
1 5 10 15  
Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly  
20 25

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

His Ile Gly His  
1

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

His Lys Asn Thr Ser Thr Leu Ser Cys Asp Gly Ser Leu Arg His Lys  
1 5 10 15  
Phe

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Arg Lys Leu Lys His Ile Asn Ile Asp Gln Phe Val Arg Lys Tyr Arg  
1 5 10 15

Ala

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Arg His Ile Gln Asn Ile Asp Ile Gln His Leu Ala Gly Lys Leu Lys  
1                      5                      10                      15  
  
Gln His

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Lys Lys Gly Phe Tyr Lys Lys Lys Gln Cys Arg Pro Ser Lys Gly Arg  
1                      5                      10                      15  
  
Lys

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Lys Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg  
1                      5                      10                      15  
  
Glu Arg

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys  
1                    5                    10                    15

Lys

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Lys Lys Thr Asn Leu Phe Ser Ala Leu Ile Lys Lys Lys Lys Lys Thr  
1                    5                    10                    15

Ala

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 17 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS:  
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Arg Lys Thr Leu Leu Asn Ser Leu Glu Glu Ala Lys Lys Lys Lys Glu  
1                    5                    10                    15

Asp

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Arg Glu Leu Asp Glu Ser Leu Gln Val Ala Glu Arg Leu Thr Arg  
1                      5                      10                      15

Lys

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Arg Arg Ser Tyr Ala Leu Val Ser Leu Ser Phe Phe Arg Lys Leu Arg  
1                      5                      10                      15

Leu

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Arg Arg Tyr Gly Asp Glu Glu Leu His Leu Cys Val Ser Arg Lys His  
1                      5                      10                      15

Phe

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Gln Asn Arg Glu Arg Arg  
1                      5                      10                      15

Arg

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

His Arg Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg Lys  
1                      5                      10                      15

Phe

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Lys Arg Pro Pro Ile Ser Asp Ser Glu Glu Leu Ser Ala Lys Lys Arg  
1                      5                      10                      15

Lys



(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

Lys Lys Gly Lys Lys Pro Lys Thr Glu Lys Glu Asp Lys Val Lys His  
1                      5                      10                      15  
  
Ile

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Arg Lys Arg Met Arg Asn Arg Ile Ala Ala Ser Lys Cys Arg Lys Arg  
1                      5                      10                      15  
  
Lys

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Arg His Ile Gln Asn Ile Asp Ile Gln His Leu Ala Gly Lys Leu Lys  
1                      5                      10                      15  
  
Gln His

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Lys Lys Ile Thr Glu Val Ala Leu Met Gly His Leu Ser Cys Asp Thr  
1                      5                      10                      15  
  
Lys Glu Glu Arg Lys  
                    20

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 14 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Lys His Ile Asn Ile Asp Gln Phe Val Arg Lys Tyr Arg Ala  
1                      5                      10

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

His Arg Asn Ile Gln Glu Tyr Leu Ser Ile Leu Thr Asp Pro Asp Gly  
1                      5                      10                      15  
  
Lys Gly Lys Glu Lys  
                    20

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Lys Glu Val Tyr Gly Phe Asn Pro Glu Gly Lys Ala Leu Leu Lys Lys  
1                      5                      10                      15

Thr Lys

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Lys Val Leu Val Asp His Phe Gly Tyr Thr Lys Asp Asp Lys His Glu  
1                      5                      10                      15

Asp Met

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Arg Gln Val Ser His Ala Lys Glu Lys Leu Thr Ala Leu Thr Lys Lys  
1                      5                      10                      15

Tyr Arg

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Lys Tyr Gln Ile Arg Ile Gln Ile Gln Glu Lys Leu Gln Gln Leu Lys  
1 5 10 15

Arg His

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Lys Tyr Gln Ile Arg Ile Gln Ile Gln Glu Lys Leu Gln Gln Leu Lys  
1 5 10 15

Arg His

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Lys Gly Met Ala Leu Phe Gly Glu Gly Lys Ala Glu Phe Thr Gly Arg  
1 5 10 15

His Asp Ala His  
20

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Lys	Gln	Ser	Phe	Asp	Leu	Ser	Val	Lys	Ala	Gln	Tyr	Lys	Lys	Asn	Lys
1				5					10					15	

His Arg

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Lys	Leu	Glu	Gly	Thr	Thr	Arg	Leu	Thr	Arg	Lys	Arg	Gly	Leu	Lys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Lys	Leu	Asp	Val	Thr	Thr	Ser	Ile	Gly	Arg	Arg	Gln	His	Leu	Arg
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Lys	Lys	Leu	Asp	Phe	Arg	Glu	Ile	Gln	Ile	Tyr	Lys	Lys	Leu	Arg
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Lys Ser Pro Ala Thr Asp Leu His Leu Arg Tyr Gln Lys Asp Lys Lys  
1                      5                      10                      15

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Lys Tyr His Trp Glu His Thr Gly Leu Thr Leu Arg Glu Val Ser Ser  
1                      5                      10                      15

Lys Leu Arg Arg  
20

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Lys Asp Asn Val Phe Asp Gly Leu Val Arg Val Thr Gln Lys Phe His  
1                      5                      10                      15

Met Lys Val Lys His  
20

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Ser	Ile	Asn	Leu	Pro	Phe	Phe	Glu	Thr	Leu	Gln	Glu	Tyr	Phe	Glu	Arg	
1				5					10					15		
Asn	Arg	Gln	Thr	Ile	Ile	Val	Val	Val	Glu	Asn	Val	Gln	Arg	Asn	Leu	
			20					25					30			
Lys	His	Ile	Asn	Ile	Asp	Gln	Phe	Val	Arg	Lys	Tyr	Arg	Ala	Ala	Leu	
		35					40					45				
Gly	Lys	Leu	Pro	Gln	Gln	Ala	Asn	Asp	Tyr	Leu	Asn	Ser	Phe	Asn	Trp	
	50					55					60					
Glu	Arg	Gln	Val	Ser	His	Ala	Lys	Glu	Lys	Leu	Thr	Ala	Leu	Thr	Lys	
65					70					75					80	
Lys	Tyr	Arg	Ile	Thr	Glu	Asn	Asp	Ile	Gln	Ile	Ala	Leu	Asp	Asp	Ala	
			85						90					95		
Lys	Ile	Asn	Phe	Asn	Glu	Lys	Leu	Ser	Gln	Leu	Gln	Thr	Tyr	Met	Ile	
			100					105						110		
Gln	Phe	Asp	Gln	Tyr	Ile	Lys	Asp	Ser	Tyr	Asp	Leu	His	Asp	Leu	Lys	
		115					120					125				
Ile	Ala	Ile	Ala	Asn	Ile	Ile	Asp	Glu	Ile	Ile	Glu	Lys	Leu	Lys	Ser	
	130					135					140					
Leu	Asp	Glu	His	Tyr	His	Ile	Arg	Val	Asn	Leu	Val	Lys	Thr	Ile	His	
145					150					155					160	
Asp	Leu	His	Leu	Phe	Ile	Glu	Asn	Ile	Asp	Phe	Asn	Lys	Ser	Gly	Ser	
			165						170					175		
Ser	Thr	Ala	Ser													
			180													

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Pro	Gln	Gln	Val	Asn	Asp	Tyr	Leu	Ser	Thr	Phe	Ser	Trp	Glu	Arg	Gln	
1				5					10					15		

Val Leu Ser Ala Lys Lys Lys His Ser Asp Phe Met Glu Asp Tyr Arg  
20 25 30

Ile Thr Glu Asn Asp Val Arg Ile Ala Leu Asp Asn Ala Lys Ile Asn  
35 40 45

Leu Asn Glu Lys Leu Thr Gln Leu Gln Thr Tyr Val Ile Gln Phe Asp  
50 55 60

Gln Tyr Ile Lys Asp Asn Tyr Asp Leu His Asp Phe Lys Thr Ala Ile  
65 70 75 80

Ala Arg Ile Ile Asp Glu Ile Ile Ala Thr Leu Lys Ile Leu  
85 90

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Lys Tyr Arg Val Ala Leu Ser Arg Leu Pro Gln Gln Ile His Asp Tyr  
1 5 10 15

Leu Asn Ala Ser Asp Trp Glu Arg Gln Val Ala Gly Ala Lys Glu Lys  
20 25 30

Leu Thr Ser Phe Met Glu Asn Tyr Arg Ile Thr Asp Asn Asp Val Leu  
35 40 45

Ile Ala Leu Asp Ser Ala Lys Ile Asn Leu Asn Glu Lys Leu Ser Gln  
50 55 60

Leu Glu Thr Tyr Ala Ile Gln Phe Asp Gln Tyr Ile Arg Asp Asn Tyr  
65 70 75 80

Asp Ala Gln Asp Leu  
85

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Leu	Asn	Asp	Phe	Gln	Val	Pro	Asp	Leu	His	Ile	Pro	Glu	Phe	Gln	Leu
1				5					10					15	
Pro	His	Ile	Ser	His	Thr	Ile	Glu	Val	Pro	Thr	Phe	Gly	Lys	Leu	Tyr
			20					25					30		
Ser	Ile	Leu	Lys	Ile	Gln	Ser	Pro	Leu	Phe	Thr	Leu	Asp	Ala	Asn	Ala
		35					40					45			
Asp	Ile	Gly	Asn	Gly	Thr	Thr	Ser	Ala	Asn	Glu	Ala	Gly	Ile	Ala	Ala
	50					55					60				
Ser	Ile	Thr	Ala	Lys	Gly	Glu	Ser	Lys	Leu	Glu	Val	Leu	Asn	Phe	Asp
65					70					75					80
Phe	Gln	Ala	Asn	Ala	Gln	Leu	Ser	Asn	Pro	Lys	Ile	Asn	Pro	Leu	Ala
				85					90					95	
Leu	Lys	Glu	Ser	Val	Lys	Phe	Ser	Ser	Lys	Tyr	Leu	Arg	Thr	Glu	His
			100					105					110		
Gly	Ser	Glu	Met	Leu	Phe	Phe	Gly	Asn	Ala	Ile	Glu	Gly	Lys	Ser	Asn
		115					120					125			
Thr	Val	Ala	Ser	Leu	His	Thr	Glu	Lys	Asn	Thr	Leu	Glu	Leu	Ser	Asn
	130					135					140				
Gly	Val	Ile	Val	Lys	Ile	Asn	Asn	Gln	Leu	Thr	Leu	Asp	Ser	Asn	Thr
145					150					155					160
Lys	Tyr	Phe	His	Lys	Leu	Asn	Ile	Pro	Lys	Leu	Asp	Phe	Ser	Ser	Gln
				165					170					175	
Ala	Asp	Leu	Arg	Asn	Glu	Ile	Lys	Thr	Leu	Leu	Lys	Ala	Gly	His	Ile
			180					185					190		
Ala	Trp	Thr	Ser	Ser	Gly	Lys	Gly	Ser	Trp	Lys	Trp	Ala	Cys	Pro	Arg
	195						200					205			
Phe	Ser	Asp	Glu	Gly	Thr	His	Glu	Ser	Gln	Ile	Ser	Phe	Thr	Ile	Glu
	210					215					220				
Gly	Pro	Leu	Thr	Ser	Phe	Gly	Leu	Ser	Asn	Lys	Ile	Asn	Ser	Lys	His
225					230					235					240
Leu	Arg	Val	Asn	Gln	Asn	Leu	Val	Tyr	Glu	Ser	Gly	Ser	Leu	Asn	Phe
				245					250					255	
Ser	Lys	Leu	Glu	Ile	Gln	Ser	Gln	Val	Asp	Ser	Gln	His	Val	Gly	His
			260					265					270		

Ser Val Leu Thr Ala Lys Gly Met Ala Leu Phe Gly Glu Gly Lys Ala  
 275 280 285

Glu Phe Thr Gly Arg His Asp Ala His Leu Asn Gly Lys Val Ile Gly  
 290 295 300

Thr Leu Lys Asn Ser Leu Phe Phe Ser Ala Gln Pro Phe Glu Ile Thr  
 305 310 315 320

Ala Ser Thr Asn Asn Glu Gly Asn Leu Lys Val Arg Phe Pro Leu Arg  
 325 330 335

Leu Thr Gly Lys Ile Asp Phe Leu Asn Asn Tyr Ala Leu Phe Leu Ser  
 340 345 350

Pro Ser Ala Gln Gln Ala Ser Trp Gln Val Ser Ala Arg Phe Asn Gln  
 355 360 365

Tyr Lys Tyr Asn Gln Asn Phe Ser Ala Gly Asn Asn Glu Asn Ile Met  
 370 375 380

Glu Ala His Val Gly Ile Asn Gly Glu Ala Asn Leu Asp Phe Leu Asn  
 385 390 395 400

Ile Pro Leu Thr Ile Pro Glu Met Arg Leu Pro Tyr Thr Ile Ile Thr  
 405 410 415

Thr Pro Pro Leu Lys Asp Phe Ser Leu Trp Glu Lys Thr Gly Leu Lys  
 420 425 430

Glu Phe Leu Lys Thr Thr Lys Gln Ser Phe Asp Leu Ser Val Lys Ala  
 435 440 445

Gln Tyr Lys Lys Asn Lys His Arg His Ser Ile Thr Asn Pro Leu Ala  
 450 455 460

Val Leu Cys Glu Phe Ile Ser Gln Ser Ile Lys Ser Phe Asp Arg His  
 465 470 475 480

Phe Glu Lys Asn Arg Asn Asn Ala Leu Asp Phe Val Thr Lys Ser Tyr  
 485 490 495

Asn Glu Thr Lys Ile Lys Phe Asp Lys Tyr Lys Ala Glu Lys Ser His  
 500 505 510

Asp Glu Leu Pro Arg Thr Phe Gln Ile Pro Gly Tyr Thr Val Pro Val  
 515 520 525

Val Asn Val Glu Val Ser Pro Phe Thr Ile Glu Met Ser Ala Phe Gly  
 530 535 540

Tyr Val Phe Pro Lys Ala Val Ser Met Pro Ser Phe Ser Ile Leu Gly  
 545 550 555 560

Ser Asp Val Arg Val Pro Ser Tyr Thr Leu Ile Leu Pro Ser Leu Glu  
 565 570 575  
 Leu Pro Val Leu His Val Pro Arg Asn Leu Lys Leu Ser Leu Pro His  
 580 585 590  
 Phe Lys Glu Leu Cys Thr Ile Ser His Ile Phe Ile Pro Ala Met Gly  
 595 600 605  
 Asn Ile Thr Tyr Asp Phe Ser Phe Lys Ser Ser Val Ile Thr Leu Asn  
 610 615 620  
 Thr Asn Ala Glu Leu Phe Asn Gln Ser Asp Ile Val Ala His Leu Leu  
 625 630 635 640  
 Ser Ser Ser Ser Ser Val Ile Asp Ala Leu Gln Tyr Lys Leu Glu Gly  
 645 650 655  
 Thr Thr Arg Leu Thr Arg Lys Arg Gly Leu Lys Leu Ala Thr Ala Leu  
 660 665 670  
 Ser Leu Ser Asn Lys Phe Val Glu Gly Ser His Asn Ser Thr Val Ser  
 675 680 685  
 Leu Thr Thr Lys Asn Met Glu Val Ser Val Ala Lys Thr Thr Lys Ala  
 690 695 700  
 Glu Ile Pro Ile Leu Arg Met Asn Phe Lys Gln Glu Leu Asn Gly Asn  
 705 710 715 720  
 Thr Lys Ser Lys Pro Thr Val Ser Ser Ser Met Glu Phe Lys Tyr Asp  
 725 730 735  
 Phe Asn Ser Ser Met Leu Tyr Ser Thr Ala Lys Gly Ala Val Asp His  
 740 745 750  
 Lys Leu Ser Leu Glu Ser Leu Thr Ser Tyr Phe Ser Ile Glu Ser Ser  
 755 760 765  
 Thr Lys Gly Asp Val Lys Gly Ser Val Leu Ser Arg Glu Tyr Ser Gly  
 770 775 780  
 Thr Ile Ala Ser Glu Ala Asn Thr Tyr Leu Asn Ser Lys Ser Thr Arg  
 785 790 795 800  
 Ser Ser Val Lys Leu Gln Gly Thr Ser Lys Ile Asp Asp Ile Trp Asn  
 805 810 815  
 Leu Glu Val Lys Glu Asn Phe Ala Gly Glu Ala Thr Leu Gln Arg Ile  
 820 825 830  
 Tyr Ser Leu Trp Glu His Ser Thr  
 835 840

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Glu Phe Gln Leu Pro Arg Leu Ser His Thr Ile Glu Ile Pro Ala Phe  
1 5 10 15  
Gly Arg Leu His Gly Ile Leu Lys Ile Gln Ser Pro Leu Phe Ile Leu  
20 25 30  
Asp Ala Asn Ala Asn Ile Gln Asn Val Thr Thr Leu Glu Asn Lys Ala  
35 40 45  
Glu Ile Val Ala Ser Ile Ala Ala Thr Gly Glu Ser Glu Ile Glu Ala  
50 55 60  
Leu Asn Phe Asp Phe Gln Ala Gln Ala Gln Phe Leu Glu Leu Asn Pro  
65 70 75 80  
Asn Pro Leu Ile Leu Lys Glu Ser Met Asn Phe Ser Ser Lys His Ala  
85 90 95  
Arg Met Glu His Glu Gly Glu Ile Leu Phe Ser Gly Lys Phe Ile Glu  
100 105 110  
Gly Lys Leu Asp Thr Val Ala Ser Leu Gln Thr Glu Lys Asn Met Val  
115 120 125  
Glu Phe Asn Asn Gly Met Ile Val Lys Ile Asn Asn Pro Ile Ile Leu  
130 135 140  
Asp Ser His Thr Lys Tyr Phe His Lys Leu Ser Ile Pro Arg Leu Asp  
145 150 155 160  
Phe Ser Ser Lys Ala Ser Phe Asn Asn Glu Ile Lys Met Leu Leu Glu  
165 170 175  
Ala Gly His Val Ala Trp Thr Ser Ser Gly Thr Gly Ser Trp Asn Trp  
180 185 190  
Ala Cys Pro Asn Phe Ser Asp Glu Gly Thr His Ser Ser Lys Ile Ser  
195 200 205  
Phe Thr Val Glu Gly Pro Ile Ala Phe Phe Gly Leu Ser Asn Asn Ile  
210 215 220

Asn Gly Lys His Leu Arg Val Ile Gln Lys Leu Ala Tyr Glu Ser Gly  
 225 230 235 240  
 Phe Leu Asn Tyr Ser Met Leu Glu Val Glu Ser Lys Val Glu Ser Gln  
 245 250 255  
 His Val Gly Ser Ser Ile Leu Thr Gly Lys Gly Thr Val Leu Leu Arg  
 260 265 270  
 Glu Ala Lys Ala Glu Met Thr Gly Glu His Asn Ala Asp Leu Asn Gly  
 275 280 285  
 Lys Val Ile Gly Thr Leu Lys Asn Ser Leu Ser Phe Ser Ala Gln Pro  
 290 295 300  
 Phe Met Ile Thr Ala Ser Thr Asn Asn Asp Gly Asn Leu Lys Val Ser  
 305 310 315 320  
 Phe Pro Leu Lys Leu Thr Gly Lys Ile Asp Phe Leu Asn Asn Tyr Ala  
 325 330 335  
 Leu Phe Leu Ser Pro His Ala Gln Gln Ala Ser Trp Gln Val Ser Ala  
 340 345 350  
 Arg Phe Asn Tyr Lys Tyr Asn Gln Asn Phe Ser Ala Ile Asn Asn Glu  
 355 360 365  
 His Asn Ile Glu Ala His Val Gly Met Asn Gly Asp Ala Asn Leu Asp  
 370 375 380  
 Phe Leu Thr Ile Pro Leu Thr Ile Pro Glu Val Lys Leu Pro Tyr Ile  
 385 390 395 400  
 Gly Leu Thr Thr Pro Leu Leu Lys Asp Phe Ser Ile Trp Glu Glu Thr  
 405 410 415  
 Gly Leu Lys Lys Gln Ser Phe Asp Leu Ser Val Lys Ala Gln Tyr Lys  
 420 425 430  
 Lys Asn Arg Asp Arg His Ser Ile Ala Ile Pro Leu Asn Gly Phe Tyr  
 435 440 445  
 Glu Phe Ile Leu Asn Asn Val Asp Ser Gly Ile Gly Lys Ile Gly Lys  
 450 455 460  
 Val Arg Asp Ser Ala Leu Asp Tyr Leu Ile Ser Ser Tyr Asn Glu Ala  
 465 470 475 480  
 Lys Asn Lys Phe Glu Asn Ser Leu Ile Gln Pro Ser Arg Thr Phe Gln  
 485 490 495  
 Lys Arg Gly Tyr Thr Ile Pro Phe Val Asn Ile Glu Val Thr Pro Phe  
 500 505 510

Thr Val Glu Thr Leu Ala Ser Ser His Val Ile Pro Lys Ala Ile Asn  
 515 520 525

Thr Pro Ser Val His Ile Leu Gly Pro Asn Val Ile Val Pro Ser Tyr  
 530 535 540

Arg Leu Val Leu Pro Ser Leu Glu Leu Pro Val Leu Arg Val Pro Arg  
 545 550 555 560

Asn Leu Leu Lys Phe Ser Leu Pro Asp Phe Lys Glu Leu Arg Thr Ile  
 565 570 575

Asp Asn Ile Tyr Ile Pro Ala Leu Gly Asn Phe Thr Tyr Asp Phe Ser  
 580 585 590

Phe Lys Ser Ser Val Ile Thr Leu Asn Thr Asn Val Gly Leu Tyr Asn  
 595 600 605

Arg Ser Asp Ile Val Ala His Phe Leu Ser Ser Ser Ser Phe Val Thr  
 610 615 620

Asp Ala Leu Gln Tyr Lys Leu Glu Gly Thr Ser Arg Leu Thr Arg Lys  
 625 630 635 640

Arg Gly Leu Lys Leu Ala Thr Ala Asp Ser Leu Thr Asn Lys Phe Val  
 645 650 655

Lys Gly Asn His Asp Ser Thr Phe Ser Leu Thr Lys Lys Asn Met Glu  
 660 665 670

Ala Ser Val Lys Thr Thr Ala Asn Leu His Ala Pro Ile Leu Thr Met  
 675 680 685

Asn Phe Lys Gln Glu Leu Asn Gly Asn Ala Lys Ser Lys Pro Ile Val  
 690 695 700

Ser Ser Ser Ile Glu Leu Asn Tyr Asp Phe Asn Ser Ser Lys Leu Tyr  
 705 710 715 720

Ser Thr Ala Lys Gly Gly Val Asp His Lys Phe Ser Leu Glu Ser Leu  
 725 730 735

Thr Ser Tyr Phe Ser Ile Glu Ser Ser Thr Lys Gly Asn Ile Lys Gly  
 740 745 750

Ser Val Leu Ser Gln Glu Tyr Ser Gly Ser Val Ala Ser Glu Ala Asn  
 755 760 765

Thr Tyr Leu Asn Ser  
 770

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 785 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Glu Phe Gln Leu Pro His Leu Ser His Thr Ile Glu Ile Pro Ala Phe  
1 5 10 15  
Gly Lys Leu His Ser Ile Leu Lys Ile Gln Ser Pro Leu Phe Ile Leu  
20 25 30  
Asp Ala Asn Ala Asn Ile Gln Asn Val Thr Thr Ser Gly Asn Lys Ala  
35 40 45  
Glu Ile Val Ala Ser Val Thr Ala Lys Gly Glu Ser Gln Phe Glu Ala  
50 55 60  
Leu Asn Phe Asp Phe Gln Ala Gln Ala Gln Phe Leu Glu Leu Asn Pro  
65 70 75 80  
His Pro Pro Val Leu Lys Glu Ser Met Asn Phe Ser Ser Lys His Val  
85 90 95  
Arg Met Glu His Glu Gly Glu Ile Val Phe Asp Gly Lys Ala Ile Glu  
100 105 110  
Gly Lys Ser Asp Thr Val Ala Ser Leu His Thr Glu Lys Asn Glu Val  
115 120 125  
Glu Phe Asn Asn Gly Met Thr Val Lys Val Asn Asn Gln Leu Thr Leu  
130 135 140  
Asp Ser His Thr Lys Tyr Phe His Lys Leu Ser Val Pro Arg Leu Asp  
145 150 155 160  
Phe Ser Ser Lys Ala Ser Leu Asn Asn Glu Ile Lys Thr Leu Leu Glu  
165 170 175  
Ala Gly His Val Ala Leu Thr Ser Ser Gly Thr Gly Ser Trp Asn Trp  
180 185 190  
Ala Cys Pro Asn Phe Ser Asp Glu Gly Ile His Ser Ser Gln Ile Ser  
195 200 205  
Phe Thr Val Asp Gly Pro Ile Ala Phe Val Gly Leu Ser Asn Asn Ile  
210 215 220  
Asn Gly Lys His Leu Arg Val Ile Gln Lys Leu Thr Tyr Glu Ser Gly  
225 230 235 240

Phe	Leu	Asn	Tyr	Ser	Lys	Phe	Glu	Val	Glu	Ser	Lys	Val	Glu	Ser	Gln	
				245					250					255		
His	Val	Gly	Ser	Ser	Ile	Leu	Thr	Ala	Asn	Gly	Arg	Ala	Leu	Leu	Lys	
			260					265					270			
Asp	Ala	Lys	Ala	Glu	Met	Thr	Gly	Glu	His	Asn	Ala	Asn	Leu	Asn	Gly	
		275					280					285				
Lys	Val	Ile	Gly	Thr	Leu	Lys	Asn	Ser	Leu	Phe	Phe	Ser	Ala	Gln	Pro	
	290					295					300					
Phe	Glu	Ile	Thr	Ala	Ser	Thr	Asn	Asn	Glu	Gly	Asn	Leu	Lys	Val	Gly	
305					310					315					320	
Phe	Pro	Leu	Lys	Leu	Thr	Gly	Lys	Ile	Asp	Phe	Leu	Asn	Asn	Tyr	Ala	
				325					330					335		
Leu	Phe	Leu	Ser	Pro	Arg	Ala	Gln	Gln	Ala	Ser	Trp	Gln	Ala	Ser	Thr	
			340					345					350			
Arg	Phe	Asn	Gln	Tyr	Lys	Tyr	Asn	Gln	Asn	Phe	Ser	Ala	Ile	Asn	Asn	
		355					360					365				
Glu	His	Asn	Ile	Glu	Ala	Ser	Ile	Gly	Met	Asn	Gly	Asp	Ala	Asn	Leu	
	370					375					380					
Asp	Phe	Leu	Asn	Ile	Pro	Leu	Thr	Ile	Pro	Glu	Ile	Asn	Leu	Pro	Tyr	
385					390					395					400	
Thr	Glu	Phe	Lys	Thr	Pro	Leu	Leu	Lys	Asp	Phe	Ser	Ile	Trp	Glu	Glu	
				405					410					415		
Thr	Gly	Leu	Lys	Glu	Phe	Leu	Lys	Thr	Thr	Lys	Gln	Ser	Phe	Asp	Leu	
			420					425					430			
Ser	Val	Lys	Ala	Gln	Tyr	Lys	Lys	Asn	Ser	Asp	Lys	His	Ser	Ile	Val	
		435					440					445				
Val	Pro	Leu	Gly	Met	Phe	Tyr	Glu	Phe	Ile	Leu	Asn	Asn	Val	Asn	Ser	
	450					455					460					
Trp	Asp	Arg	Lys	Phe	Glu	Lys	Val	Arg	Asn	Asn	Ala	Leu	His	Phe	Leu	
465					470					475					480	
Thr	Thr	Ser	Tyr	Asn	Glu	Ala	Lys	Ile	Lys	Val	Asp	Lys	Tyr	Lys	Thr	
				485					490					495		
Glu	Asn	Ser	Leu	Asn	Gln	Pro	Ser	Gly	Thr	Phe	Gln	Asn	His	Gly	Tyr	
			500					505					510			
Thr	Ile	Pro	Val	Val	Asn	Ile	Glu	Val	Ser	Pro	Phe	Ala	Val	Glu	Thr	
			515				520					525				



Leu Ala Ser Arg His Val Ile Pro Thr Ala Ile Ser Thr Pro Ser Val  
 530 535 540  
 Thr Ile Pro Gly Pro Asn Ile Met Val Pro Ser Tyr Lys Leu Val Leu  
 545 550 555 560  
 Pro Pro Leu Glu Leu Pro Val Phe His Gly Pro Gly Asn Leu Phe Lys  
 565 570 575  
 Phe Phe Leu Pro Asp Phe Lys Gly Phe Asn Thr Ile Asp Asn Ile Tyr  
 580 585 590  
 Ile Pro Ala Met Gly Asn Phe Thr Tyr Asp Phe Ser Phe Lys Ser Ser  
 595 600 605  
 Val Ile Thr Leu Asn Thr Asn Ala Gly Leu Tyr Asn Gln Ser Asp Ile  
 610 615 620  
 Val Ala His Phe Leu Ser Ser Ser Ser Phe Val Thr Asp Ala Leu Gln  
 625 630 635 640  
 Tyr Lys Leu Glu Gly Thr Ser Arg Leu Met Arg Lys Arg Gly Leu Lys  
 645 650 655  
 Leu Ala Thr Ala Val Ser Leu Thr Asn Lys Phe Val Lys Gly Ser His  
 660 665 670  
 Asp Ser Thr Ile Ser Leu Thr Lys Lys Asn Met Glu Ala Ser Val Arg  
 675 680 685  
 Thr Thr Ala Asn Leu His Ala Pro Ile Phe Ser Met Asn Phe Lys Gln  
 690 695 700  
 Glu Leu Asn Gly Asn Thr Lys Ser Lys Pro Thr Val Ser Ser Ser Ile  
 705 710 715 720  
 Glu Leu Asn Tyr Asp Phe Asn Ser Ser Lys Leu His Ser Thr Ala Thr  
 725 730 735  
 Gly Gly Ile Asp His Lys Phe Ser Leu Glu Ser Leu Thr Ser Tyr Phe  
 740 745 750  
 Ser Ile Glu Ser Phe Thr Lys Gly Asn Ile Lys Ser Ser Phe Leu Ser  
 755 760 765  
 Gln Glu Tyr Ser Gly Ser Val Ala Asn Glu Ala Asn Val Tyr Leu Asn  
 770 775 780  
 Ser  
 785

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Glu	Tyr	Ser	Gly	Thr	Ile	Ala	Ser	Glu	Ala	Asn	Thr	Tyr	Leu	Asn	Ser		
1				5				10					15				
Lys	Ser	Thr	Arg	Ser	Ser	Val	Lys	Leu	Gln	Gly	Thr	Ser	Lys	Ile	Asp		
			20				25						30				
Asp	Ile	Trp	Asn	Leu	Glu	Val	Lys	Glu	Asn	Phe	Ala	Gly	Glu	Ala	Thr		
			35				40					45					
Leu	Gln	Arg	Ile	Tyr	Ser	Leu	Trp	Glu	His	Ser	Thr	Lys	Asn	His	Leu		
	50					55					60						
Gln	Leu	Glu	Gly	Leu	Phe	Phe	Thr	Asn	Gly	Glu	His	Thr	Ser	Lys	Ala		
65				70					75						80		
Thr	Leu	Glu	Leu	Ser	Pro	Trp	Gln	Met	Ser	Ala	Leu	Val	Gln	Val	His		
				85					90					95			
Ala	Ser	Gln	Pro	Ser	Ser	Phe	His	Asp	Phe	Pro	Asp	Leu	Gly	Gln	Glu		
			100					105					110				
Val	Ala	Leu	Asn	Ala	Asn	Thr	Lys	Asn	Gln	Lys	Ile	Arg	Trp	Lys	Asn		
			115				120					125					
Glu	Val	Arg	Ile	His	Ser	Gly	Ser	Phe	Gln	Ser	Gln	Val	Glu	Leu	Ser		
	130					135					140						
Asn	Asp	Gln	Glu	Lys	Ala	His	Leu	Asp	Ile	Ala	Gly	Ser	Leu	Glu	Gly		
145				150						155				160			
His	Leu	Arg	Phe	Leu	Lys	Asn	Ile	Ile	Leu	Pro	Val	Tyr	Asp	Lys	Ser		
			165						170					175			
Leu	Trp	Asp	Phe	Leu	Lys	Leu	Asp	Val	Thr	Thr	Ser	Ile	Gly	Arg	Arg		
			180					185					190				
Gln	His	Leu	Arg	Val	Ser	Thr	Ala	Phe	Val	Tyr	Thr	Lys	Asn	Pro	Asn		
			195				200					205					
Gly	Tyr	Ser	Phe	Ser	Ile	Pro	Val	Lys	Val	Leu	Ala	Asp	Lys	Phe	Ile		
	210					215				220							
Thr	Pro	Gly	Leu	Lys	Leu	Asn	Asp	Leu	Asn	Ser	Val	Leu	Val	Met	Pro		
225					230					235				240			

Thr Phe His Val Pro Phe Thr Asp Leu Gln Val Pro Ser Cys Lys Leu  
 245 250 255  
 Asp Phe Arg Glu Ile Gln Ile Tyr Lys Lys Leu Arg Thr Ser Ser Phe  
 260 265 270  
 Ala Leu Asn Leu Pro Thr Leu Pro Glu Val Lys Phe Pro Glu Val Asp  
 275 280 285  
 Val Leu Thr Lys Tyr Ser Gln Pro Glu Asp Ser Leu Ile Pro Phe Phe  
 290 295 300  
 Glu Ile Thr Val Pro Glu Ser Gln Leu Thr Val Ser Gln Phe Thr Leu  
 305 310 315 320  
 Pro Lys Ser Val Ser Asp Gly Ile Ala Ala Leu Asp Leu Asn Ala Val  
 325 330 335  
 Ala Asn Lys Ile Ala Asp Phe Glu Leu Pro Thr Ile Ile Val Pro Glu  
 340 345 350  
 Gln Thr Ile Glu Ile Pro Ser Ile Lys Phe Ser Val Pro Ala Gly Ile  
 355 360 365  
 Val Ile Pro Ser Phe Gln Ala Leu Thr Ala Arg Phe Glu Val Asp Ser  
 370 375 380  
 Pro Val Tyr Asn Ala Thr Trp Ser Ala Ser Leu Lys Asn Lys Ala Asp  
 385 390 395 400  
 Tyr Val Glu Thr Val Leu Asp Ser Thr Cys Ser Ser Thr Val Gln Phe  
 405 410 415  
 Leu Glu Tyr Glu Leu Asn Val Leu Gly Thr His Lys Ile Glu Asp Gly  
 420 425 430  
 Thr Leu Ala Ser Lys Thr Lys Gly Thr Leu Ala His Arg Asp Phe Ser  
 435 440 445  
 Ala Glu Tyr Glu Glu Asp Gly Lys Phe Glu Gly Leu Gln Glu Trp Glu  
 450 455 460  
 Gly Lys Ala His Leu Asn Ile Lys Ser Pro Ala Phe Thr Asp Leu His  
 465 470 475 480  
 Leu Arg Tyr Gln Lys Asp Lys Lys Gly Ile Ser Thr Ser Ala Ala Ser  
 485 490 495  
 Pro Ala Val Gly Thr Val Gly Met Asp Met Asp Glu Asp Asp Asp Phe  
 500 505 510  
 Ser Lys Trp Asn Phe Tyr Tyr Ser Pro Gln Ser Ser Pro Asp Lys Lys  
 515 520 525

Leu Thr Ile Phe Lys Thr Glu Leu Arg Val Arg Glu Ser Asp Glu Glu  
 530 535 540

Thr Gln Ile Lys Val Asn Trp Glu Glu Glu Ala Ala Ser Gly Leu Leu  
 545 550 555 560

Thr Ser Leu Lys Asp Asn Val Pro Lys Ala Thr Gly Val Leu Tyr Asp  
 565 570 575

Tyr Val Asn Lys Tyr His Trp Glu His Thr Gly Leu Thr Leu Arg Glu  
 580 585 590

Val Ser Ser Lys Leu Arg Arg Asn Leu Gln Asn Asn Ala Glu Trp Val  
 595 600 605

Tyr Gln Gly Ala Ile Arg Gln Ile Asp Asp Ile Asp Val Arg Phe Gln  
 610 615 620

Lys Ala Ala Ser Gly Thr Thr Gly Thr Tyr Gln Glu Trp Lys Asp Lys  
 625 630 635 640

Ala Gln Asn Leu Tyr Gln Glu Leu Leu Thr Gln Glu Gly Gln Ala Ser  
 645 650 655

Phe Gln Gly Leu Lys Asp Asn Val Phe Asp Gly Leu Val Arg Val Thr  
 660 665 670

Gln Lys Phe His Met Lys Val Lys His Leu Ile Asp Ser Leu Ile Asp  
 675 680 685

Phe Leu Asn Phe Pro Arg Phe Gln Phe Pro Gly Lys Pro Gly Ile Tyr  
 690 695 700

Thr Arg Glu Glu Leu Cys Thr Met Phe Ile Arg Glu Val Gly Thr Val  
 705 710 715 720

Leu Ser Gln Val Tyr Ser Lys Val His Asn Gly Ser Glu Ile Leu Phe  
 725 730 735

Ser Tyr Phe Gln Asp Leu Val Ile Thr Leu Pro Phe Glu Leu Arg Lys  
 740 745 750

His Lys Leu Ile Asp Val Ile Ser Met Tyr Arg Glu Leu Leu Lys Asp  
 755 760 765

Leu Ser Lys Glu Ala Gln Glu Val Phe Lys Ala Ile Gln Ser Leu Lys  
 770 775 780

Thr Thr Glu Val Leu Arg Asn Leu Gln Asp Leu Leu Gln Phe Ile Phe  
 785 790 795 800

Gln Leu Ile Glu Asp Asn Ile Lys Gln Leu Lys Glu Met Lys Phe Thr  
 805 810 815

Tyr Leu Ile Asn Tyr Ile Gln Asp Glu Ile Asn Thr Ile Phe Asn Asp  
 820 825 830  
 Tyr Ile Pro Tyr Val Phe Lys Leu Leu Lys Glu Asn Leu Cys Leu Asn  
 835 840 845  
 Leu His Lys Phe Asn Glu Phe Ile Gln Asn Glu Leu Gln Glu Ala Ser  
 850 855 860  
 Gln Glu Leu Gln Gln Ile His Gln Tyr Ile Met Ala Leu Arg Glu Glu  
 865 870 875 880  
 Tyr Phe Asp Pro Ser Ile Val Gly Trp Thr Val Lys Tyr Tyr Glu Leu  
 885 890 895  
 Glu Glu Lys Ile Val Ser Leu Ile Lys Asn Leu Leu Val Ala Leu Lys  
 900 905 910  
 Asp Phe His Ser Glu Tyr Ile Val Ser Ala Ser Asn Phe Thr Ser Gln  
 915 920 925  
 Leu Ser Ser Gln Val Glu Gln Phe Leu His Arg Asn Ile Gln Glu Tyr  
 930 935 940  
 Leu Ser Ile Leu Thr Asp Pro Asp Gly Lys Gly Lys Glu Lys Ile Ala  
 945 950 955 960  
 Glu Leu Ser Ala Thr Ala Gln Glu Ile Ile Lys Ser Gln Ala Ile Ala  
 965 970 975  
 Thr Lys Lys Ile Ile Ser Asp Tyr His Gln Gln Phe Arg Tyr Lys Leu  
 980 985 990  
 Gln Asp Phe Ser Asp Gln Leu Ser Asp Tyr Tyr Glu Lys Phe Ile Ala  
 995 1000 1005  
 Glu Ser Lys Arg Leu Ile Asp Leu Ser Ile Gln Asn Tyr His Thr Phe  
 1010 1015 1020  
 Leu Ile Tyr Ile Thr Glu Leu Leu Lys Lys Leu Gln Ser Thr Thr Val  
 1025 1030 1035 1040  
 Met Asn Pro Tyr Met Lys Leu Ala Pro Gly Glu Leu Thr Ile Ile Leu  
 1045 1050 1055

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Asn	Ser	Lys	Gly	Thr	Arg	Ser	Ser	Val	Arg	Leu	Gln	Gly	Ala	Ser	Asn	
1				5					10					15		
Phe	Ala	Gly	Ile	Trp	Asn	Phe	Glu	Val	Gly	Glu	Asn	Phe	Ala	Gly	Glu	
			20					25					30			
Ala	Thr	Leu	Arg	Arg	Ile	Tyr	Gly	Thr	Trp	Glu	His	Asn	Met	Ile	Asn	
		35					40					45				
His	Leu	Gln	Val	Phe	Ser	Tyr	Phe	Asp	Thr	Lys	Gly	Lys	Gln	Thr	Cys	
	50					55					60					
Arg	Ala	Thr	Leu	Glu	Leu	Ser	Pro	Trp	Thr	Met	Ser	Thr	Leu	Leu	Gln	
65						70				75					80	
Val	His	Val	Ser	Gln	Pro	Ser	Pro	Leu	Phe	Asp	Leu	His	His	Phe	Asp	
				85					90					95		
Gln	Glu	Val	Ile	Leu	Lys	Ala	Ser	Thr	Lys	Asn	Gln	Lys	Val	Ser	Trp	
			100					105					110			
Lys	Ser	Glu	Val	Gln	Val	Glu	Ser	Gln	Val	Leu	Gln	His	Asn	Ala	His	
		115					120					125				
Phe	Ser	Asn	Asp	Gln	Glu	Glu	Val	Arg	Leu	Asp	Ile	Ala	Gly	Ser	Leu	
	130						135				140					
Glu	Gly	Gln	Leu	Trp	Asp	Leu	Glu	Asn	Phe	Phe	Leu	Pro	Ala	Phe	Gly	
145					150					155					160	
Lys	Ser	Leu	Arg	Glu	Leu	Leu	Gln	Ile	Asp	Gly	Lys	Arg	Gln	Tyr	Leu	
				165					170					175		
Gln	Ala	Ser	Thr	Ser	Leu	His	Tyr	Thr	Lys	Asn	Pro	Asn	Gly	Tyr	Leu	
			180						185				190			
Leu	Ser	Leu	Pro	Val	Gln	Glu	Leu	Thr	Asp	Arg	Phe	Ile	Ile	Pro	Gly	
		195					200					205				
Leu	Lys	Leu	Asn	Asp	Phe	Ser	Gly	Ile	Lys	Ile	Tyr	Lys	Lys	Leu	Ser	
	210						215				220					
Thr	Ser	Pro	Phe	Ala	Leu	Asn	Leu	Thr	Met	Leu	Pro	Lys	Val	Lys	Phe	
225					230					235					240	
Pro	Gly	Val	Asp	Leu	Leu	Thr	Gln	Tyr	Ser	Lys	Pro	Glu	Gly	Ser	Ser	
				245					250					255		
Val	Pro	Thr	Phe	Glu	Thr	Thr	Ile	Pro	Glu	Ile	Gln	Leu	Thr	Val	Ser	
			260					265				270				

Gln Phe Thr Leu Pro Lys Ser Phe Pro Val Gly Asn Thr Val Phe Asp  
 275 280 285  
 Leu Asn Lys Leu Thr Asn Leu Ile Ala Asp Val Asp Leu Pro Ser Ile  
 290 295 300  
 Thr Leu Pro Glu Gln Thr Ile Glu Ile Pro Ser Leu Glu Phe Ser Val  
 305 310 315 320  
 Pro Ala Gly Ile Phe Ile Pro Phe Phe Gly Glu Leu Thr Ala His Val  
 325 330 335  
 Gly Met Ala Ser Pro Leu Tyr Asn Val Thr Trp Ser Thr Gly Trp Lys  
 340 345 350  
 Asn Lys Ala Asp His Val Glu Thr Phe Leu Asp Ser Thr Cys Ser Ser  
 355 360 365  
 Thr Leu Gln Phe Leu Glu Tyr Ala Leu Lys Val Val Gly Thr His Arg  
 370 375 380  
 Ile Glu Asn Asp Lys Phe Ile Tyr Lys Ile Lys Gly Thr Leu Gln His  
 385 390 395 400  
 Cys Asp Phe Asn Val Lys Tyr Asn Glu Asp Gly Ile Phe Glu Gly Leu  
 405 410 415  
 Trp Asp Leu Glu Gly Glu Ala His Leu Asp Ile Thr Ser Pro Ala Leu  
 420 425 430  
 Thr Asp Phe His Leu His Tyr Lys Glu Asp Lys Thr Ser Val Ser Ala  
 435 440 445  
 Ser Ala Ala Ser Pro Ala Ile Gly Thr Val Ser Leu Asp Ala Ser Thr  
 450 455 460  
 Asp Asp Gln Ser Val Arg Leu His Val Tyr Phe Arg Pro Gln Ser Pro  
 465 470 475 480  
 Pro Asp Asn Lys Leu Ser Ile Phe Lys Met Glu Trp Arg Asp Lys Glu  
 485 490 495  
 Ser Asp Gly Glu Thr Tyr Ile Lys Ile Asn Trp Glu Glu Glu Ala Ala  
 500 505 510  
 Phe Arg Leu Leu Asp Ser Leu Lys Ser Asn Val Pro Lys Ala Ser Glu  
 515 520 525  
 Ala Val Tyr Asp Tyr Val Lys Lys Tyr His Leu Gly His Ala Ser Ser  
 530 535 540  
 Glu Leu Arg Lys Ser Leu Gln Asn Asp Ala Glu His Ala Ile Arg Met  
 545 550 555 560

Val Asp Glu Met Asn Val Asn Ala Gln Arg Val Thr Arg Asp Thr Tyr  
 565 570 575  
 Gln Ser Leu Tyr Lys Lys Met Leu Ala Gln Glu Ser Gln Ser Ile Pro  
 580 585 590  
 Glu Lys Leu Lys Lys Met Val Leu Gly Ser Leu Val Arg Ile Thr Gln  
 595 600 605  
 Lys Tyr His Met Ala Val Thr Trp Leu Met Asp Ser Val Ile His Phe  
 610 615 620  
 Leu Lys Phe Asn Arg Val Gln Phe Pro Gly Asn Ala Gly Thr Tyr Thr  
 625 630 635 640  
 Val Asp Glu Leu Tyr Thr Ile Ala Met Arg Glu Thr Lys Lys Leu Leu  
 645 650 655  
 Ser Gln Leu Phe Asn Gly Leu Gly His Leu Phe Ser Tyr Val Gln Asp  
 660 665 670  
 Gln Val Glu Lys Ser Arg Val Ile Asn Asp Ile Thr Phe Lys Cys Pro  
 675 680 685  
 Phe Ser Pro Thr Pro Cys Lys Leu Lys Asp Val Leu Leu Ile Phe Arg  
 690 695 700  
 Glu Asp Leu Asn Ile Leu Ser Asn Leu Gly Gln Gln Asp Ile Asn Phe  
 705 710 715 720  
 Thr Thr Ile Leu Ser Asp Phe Gln Ser Phe Leu Glu Arg Leu Leu Asp  
 725 730 735  
 Ile Ile Glu Glu Lys Ile Glu Cys Leu Lys Asn Asn Glu Ser Thr Cys  
 740 745 750  
 Val Pro Asp His Ile Asn Met Phe Phe Lys Thr His Ile Pro Phe Ala  
 755 760 765  
 Phe Lys Ser Leu Arg Glu Asn Ile Tyr Ser Val Phe Ser Glu Phe Asn  
 770 775 780  
 Asp Phe Val Gln Ser Ile Leu Gln Glu Gly Ser Tyr Lys Leu Gln Gln  
 785 790 795 800  
 Val His Gln Tyr Met Lys Ala Phe Arg Glu Glu Tyr Phe Asp Pro Ser  
 805 810 815  
 Val Val Gly Trp Thr Val Lys Tyr Tyr Glu Ile Glu Glu Lys Met Val  
 820 825 830  
 Asp Leu Ile Lys Thr Leu Leu Ala Pro Leu Arg Asp Phe Tyr Ser Glu  
 835 840 845



Tyr Ser Val Thr Ala Ala Asp Phe Ala Ser Lys Met Ser Thr Gln Val  
 850 855 860  
 Glu Gln Phe Val Ser Arg Asp Ile Arg Glu Tyr Leu Ser Met Leu Ala  
 865 870 875 880  
 Asp Ile Asn Gly Lys Gly Arg Glu Lys Val Ala Glu Leu Ser Ile Val  
 885 890 895  
 Val Lys Glu Arg Ile Lys Ser Trp Ser Thr Ala Val Ala Glu Ile Thr  
 900 905 910  
 Ser Asp Tyr Leu Arg Gln Leu His Ser Lys Leu Gln Asp Phe Ser Asp  
 915 920 925  
 Gln Leu Ser Gly Tyr Tyr Glu Lys Phe Val Ala Glu Ser Thr Arg Leu  
 930 935 940  
 Ile Asp Leu Ser Ile Gln Asn Tyr His Met Phe Leu Arg Tyr Ile Ala  
 945 950 955 960  
 Glu Leu Leu Lys Lys Leu Gln Val Ala Thr Ala Asn Asn Val Ser Pro  
 965 970 975  
 Tyr Leu Arg Phe Ala Gln Gly Glu Leu Ile Ile Thr Phe  
 980 985

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Lys Asp Asn Val Phe Asp Gly Leu Val Arg Val Thr Gln Lys Phe His  
 1 5 10 15  
 Met Lys Val Lys His Leu Ile Asp Ser Leu Ile Asp Phe Leu Asn Phe  
 20 25 30  
 Pro Arg Phe Gln Phe Pro Gly Lys Pro Gly Ile Tyr Thr Arg Glu Glu  
 35 40 45  
 Leu Cys Thr Met Phe Ile Arg Glu Val Gly Thr Val Leu Ser Gln Val  
 50 55 60  
 Tyr Ser Lys Val His Asn Gly Ser Glu Ile Leu Phe Ser Tyr Phe Gln  
 65 70 75 80

Asp Leu Val Ile Thr Leu Pro Phe Glu Leu Arg Lys His Lys Leu Ile  
 85 90 95

Asp Val Ile Ser Met Tyr Arg Glu Leu Leu Lys Asp Leu Ser Lys Glu  
 100 105 110

Ala Gln Glu Val Phe Lys Ala Ile Gln Ser Leu Lys Thr Thr Glu Val  
 115 120 125

Leu Arg Asn Leu Gln Asp Leu Leu Gln Phe Ile Phe Gln Leu Ile Glu  
 130 135 140

Asp Asn Ile Lys Gln Leu Lys Glu Met Lys Phe Thr Tyr Leu Ile Asn  
 145 150 155 160

Tyr Ile Gln Asp Glu Ile Asn Thr Ile Phe Asn Asp Tyr Ile Pro Tyr  
 165 170 175

Val Phe Lys Leu Leu Lys Glu Asn Leu Cys Leu Asn Leu His Lys Phe  
 180 185 190

Asn Glu Phe Ile Gln Asn Glu Leu Gln Glu Ala Ser Gln Glu Leu Gln  
 195 200 205

Gln Ile His Gln Tyr Ile Met Ala Leu Arg Glu Glu Tyr Phe Asp Pro  
 210 215 220

Ser Ile Val Gly Trp Thr Val Lys Tyr Tyr Glu Leu Glu Glu Lys Ile  
 225 230 235 240

Val Ser Leu Ile Lys Asn Leu Leu Val Ala Leu Lys Asp Phe His Ser  
 245 250 255

Glu Tyr Ile Val Ser Ala Ser Asn Phe Thr Ser Gln Leu Ser Ser Gln  
 260 265 270

Val Glu Gln Phe Leu His Arg Asn Ile Gln Glu Tyr Leu Ser Ile Leu  
 275 280 285

Thr Asp Pro Asp Gly Lys Gly Lys Glu Lys Ile Ala Glu Leu Ser Ala  
 290 295 300

Thr Ala Gln Glu Ile Ile Lys Ser Gln Ala Ile Ala Thr Lys Lys Ile  
 305 310 315 320

Ile Ser Asp Tyr His Gln Gln Phe Arg Tyr Lys Leu Gln Asp Phe Ser  
 325 330 335

Asp Gln Leu Ser Asp Tyr Tyr Glu Lys Phe Ile Ala Glu Ser Lys Arg  
 340 345 350

Leu Ile Asp Leu Ser Ile Gln Asn Tyr His Thr Phe Leu Ile Tyr Ile  
 355 360 365

Thr Glu Leu Leu Lys Lys Leu Gln Ser Thr Thr Val Met Asn Pro Tyr  
 370 375 380

Met Lys Leu Ala Pro Gly Glu Leu Thr Ile Ile Leu  
 385 390 395

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Ile Pro Gly Leu Ser Glu Lys Tyr Thr Gly Glu Glu Leu Tyr Leu Met  
 1 5 10 15

Thr Thr Glu Lys Ala Ala Lys Thr Ala Asp Ile Cys Leu Ser Lys Leu  
 20 25 30

Gln Glu Tyr Phe Asp Ala Leu Ile Ala Ala Ile Ser Glu Leu Glu Val  
 35 40 45

Arg Val Pro Ala Ser Glu Thr Ile Leu Arg Gly Arg Asn Val Leu Asp  
 50 55 60

Gln Ile Lys Glu Met Leu Lys His Leu Gln Glu Lys Ile Arg Gln Thr  
 65 70 75 80

Phe Val Thr Leu Gln Glu Ala Asp Phe Ala Gly Lys Leu Asn Arg Leu  
 85 90 95

Lys Gln Val Val Gln Lys Thr Phe Gln Lys Ala Gly Asn Met Val Arg  
 100 105 110

Ser Leu Gln Ser Lys Asn Phe Glu Asp Ile Lys Val Gln Met Gln Gln  
 115 120 125

Leu Tyr Lys Asp Ala Met Ala Ser Asp Tyr Ala His Lys Leu Arg Ser  
 130 135 140

Leu Ala Glu Asn Val Lys Lys Tyr Ile Ser Gln Ile Lys Asn Phe Ser  
 145 150 155 160

Gln Lys Thr Leu Gln Lys Leu Ser Glu Asn Leu Gln Gln Leu Val Leu  
 165 170 175

Tyr Ile Lys Ala Leu Arg Glu Glu Tyr Phe Asp Pro Thr Thr Leu Gly  
 180 185 190

Trp Ser Val Lys Tyr Tyr Glu Val Glu Asp Lys Val Leu Gly Leu Leu  
 195 200 205  
 Lys Asn Leu Met Asp Thr Leu Val Ile Trp Tyr Asn Glu Tyr Ala Lys  
 210 215 220  
 Asp Leu Ser Asp Leu Val Thr Arg Leu Thr Asp Gln Val Arg Glu Leu  
 225 230 235 240  
 Val Glu Asn Tyr Arg Gln Glu Tyr Tyr Asp Leu Ile Thr Asp Val Glu  
 245 250 255  
 Gly Lys Gly Arg Gln Lys Val Met Glu Leu Ser Ser Ala Ala Gln Glu  
 260 265 270  
 Lys Ile Arg Tyr Trp Ser Ala Val Ala Lys Arg Lys Ile Asn Glu His  
 275 280 285  
 Asn Arg Gln Val Lys Ala Lys Leu Gln Glu Ile Tyr Gly Gln Leu Ser  
 290 295 300  
 Asp Ser Gln Glu Lys Leu Ile Asn Val Ala Lys Met Leu Ile Asp Leu  
 305 310 315 320  
 Thr Val Glu Lys Tyr Ser Thr Phe Met Lys Tyr Ile Phe Glu Leu Leu  
 325 330 335  
 Arg Trp Phe Glu Gln Ala Thr Ala Asp Ser Ile Lys Pro Tyr Ile Ala  
 340 345 350  
 Val Arg Glu Gly Glu Leu Arg Ile Asp Val Pro Phe Asp Trp Glu Tyr  
 355 360 365  
 Ile Asn Gln Met Pro Gln Lys Ser Arg Glu Ala Leu Arg Asn Lys Val  
 370 375 380  
 Glu Leu Thr Arg Ala Leu Ile Gln Gln Gly Val Glu Gln Gly Thr Arg  
 385 390 395 400  
 Lys Trp Glu Glu Met Gln Ala Phe Ile Asp Glu Gln Leu Ala Thr Glu  
 405 410 415  
 Gln Leu Ser Phe Gln Gln Ile Val Glu Asn Ile Gln Lys Arg Met Lys  
 420 425 430  
 Thr

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

- (C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Asp	Met	Thr	Phe	Ser	Lys	Gln	Asn	Ala	Leu	Leu	Arg	Ser	Glu	Tyr	Gln	1	5	10	15
Ala	Asp	Tyr	Glu	Ser	Leu	Arg	Phe	Phe	Ser	Leu	Leu	Ser	Gly	Ser	Leu	20	25	30	
Asn	Ser	His	Gly	Leu	Glu	Leu	Asn	Ala	Asp	Ile	Leu	Gly	Thr	Asp	Lys	35	40	45	
Ile	Asn	Ser	Gly	Ala	His	Lys	Ala	Thr	Leu	Arg	Ile	Gly	Gln	Asp	Gly	50	55	60	
Ile	Ser	Thr	Ser	Ala	Thr	Thr	Asn	Leu	Lys	Cys	Ser	Leu	Leu	Val	Leu	65	70	75	80
Glu	Asn	Glu	Leu	Asn	Ala	Glu	Leu	Gly	Leu	Ser	Gly	Ala	Ser	Met	Lys	85	90	95	
Leu	Thr	Thr	Asn	Gly	Arg	Phe	Arg	Glu	His	Asn	Ala	Lys	Phe	Ser	Leu	100	105	110	
Asp	Gly	Lys	Ala	Ala	Leu	Thr	Glu	Leu	Ser	Leu	Gly	Ser	Ala	Tyr	Gln	115	120	125	
Ala	Met	Ile	Leu	Gly	Val	Asp	Ser	Lys	Asn	Ile	Phe	Asn	Phe	Lys	Val	130	135	140	
Ser	Gln	Glu	Gly	Leu	Lys	Leu	Ser	Asn	Asp	Met	Met	Gly	Ser	Tyr	Ala	145	150	155	160
Glu	Met	Lys	Phe	Asp	His	Thr	Asn	Ser	Leu	Asn	Ile	Ala	Gly	Leu	Ser	165	170	175	
Leu	Asp	Phe	Ser													180			

(2) INFORMATION FOR SEQ ID NO:222:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 142 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Asp	Leu	Thr	Phe	Ser	Lys	Gln	Asn	Ala	Leu	Leu	Arg	Ala	Glu	Tyr	Gln	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Ala	Asp	Tyr	Lys	Ser	Leu	Arg	Phe	Phe	Thr	Leu	Leu	Ser	Gly	Leu	Leu	20	25	30
Asn	Thr	His	Gly	Leu	Glu	Leu	Asn	Ala	Asp	Ile	Leu	Gly	Thr	Asp	Lys	35	40	45
Met	Asn	Thr	Ala	Ala	His	Lys	Ala	Thr	Leu	Arg	Ile	Gly	Gln	Asn	Gly	50	55	60
Val	Ser	Thr	Ser	Ala	Thr	Thr	Ser	Leu	Arg	Tyr	Ser	Pro	Leu	Met	Leu	65	70	75
Glu	Asn	Glu	Leu	Asn	Ala	Glu	Leu	Ala	Leu	Ser	Gly	Ala	Ser	Met	Lys	85	90	95
Leu	Ala	Thr	Asn	Gly	Arg	Phe	Lys	Glu	His	Asn	Ala	Lys	Phe	Ser	Leu	100	105	110
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Glu	Leu	Ser	Leu	Gly	Ser	Ala	Tyr	Gln	115	120	125
Ala	Met	Ile	Leu	Gly	Ala	Asp	Ser	Lys	Asn	Ile	Phe	Asn	Phe			130	135	140

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

His	Ile	Phe	Ile	Pro	Ala	Met	Gly	Asn	Ile	Thr	Tyr	Asp	Phe	Ser	Phe	1	5	10	15
Lys	Ser	Ser	Val	Ile	Thr	Leu	Asn	Thr	Asn	Ala	Glu	Leu	Phe	Asn	Gln	20	25	30	
Ser	Asp	Ile	Val	Ala	His	Leu	Leu	Ser	Ser	Ser	Ser	Ser	Val	Ile	Asp	35	40	45	
Ala	Leu	Gln	Tyr	Lys	Leu	Glu	Gly	Thr	Thr	Arg	Leu	Thr	Arg	Lys	Arg	50	55	60	
Gly	Leu	Lys	Leu	Ala	Thr	Ala	Leu	Ser	Leu	Ser	Asn	Lys	Phe	Val	Glu	65	70	75	80
Gly	Ser	His	Asn	Ser	Thr	Val	Ser	Leu	Thr	Thr	Lys	Asn	Met	Glu	Val	85	90	95	

Ser Val Ala Lys Thr Thr Lys Ala Glu Ile Pro Ile Leu Arg Met Asn  
 100 105 110  
 Phe Lys Gln Glu Leu Asn Gly Asn Thr Lys Ser Lys Pro Thr Val Ser  
 115 120 125  
 Ser Ser Met Glu Phe Lys Tyr Asp Phe Asn Ser Ser Met Leu Tyr Ser  
 130 135 140  
 Thr Ala Lys Gly Ala Val Asp His Lys Leu Ser Leu Glu Ser Leu Thr  
 145 150 155 160  
 Ser Tyr Phe Ser Ile Glu Ser Ser Thr Lys Gly Asp Val Lys Gly Ser  
 165 170 175  
 Val Leu Ser Arg Glu Tyr Ser Gly Thr Ile Ala Ser Glu Ala Asn Thr  
 180 185 190  
 Tyr Leu Asn Ser Lys Ser Thr Arg Ser Ser Val Lys Leu Gln Gly Thr  
 195 200 205  
 Ser Lys Ile Asp Asp Ile Trp Asn Leu Glu Val Lys Glu Asn Phe Ala  
 210 215 220  
 Gly Glu Ala Thr Leu Gln Arg Ile Tyr Ser Leu Trp Glu His Ser Thr  
 225 230 235 240  
 Lys Asn His Leu Gln Leu Glu Gly Leu Phe Phe Thr Asn Gly Glu His  
 245 250 255  
 Thr Ser Lys Ala Thr Leu Glu Leu Ser Pro Trp Gln Met Ser Ala Leu  
 260 265 270  
 Val Gln Val His Ala Ser Gln Pro Ser Ser Phe His Asp Phe Pro Asp  
 275 280 285  
 Leu Gly Gln Glu Val Ala Leu Asn Ala Asn Thr Lys Asn Gln Lys Ile  
 290 295 300  
 Arg Trp Lys Asn Glu Val Arg Ile His Ser Gly Ser Phe Gln Ser Gln  
 305 310 315 320  
 Val Glu Leu Ser Asn Asp Gln Glu Lys Ala His Leu Asp Ile Ala Gly  
 325 330 335  
 Ser Leu Glu Gly His Leu Arg Phe Leu Lys Asn Ile Ile Leu Pro Val  
 340 345 350  
 Tyr Asp Lys Ser Leu Trp Asp Phe Leu Lys Leu Asp Val Thr Thr Ser  
 355 360 365  
 Ile Gly Arg Arg Gln His Leu Arg Val Ser Thr Ala Phe Val Tyr Thr  
 370 375 380

Lys Asn Pro Asn Gly Tyr Ser Phe Ser Ile Pro Val Lys Val Leu Ala  
 385 390 395 400  
 Asp Lys Phe Ile Thr Pro Gly Leu Lys Leu Asn Asp Leu Asn Ser Val  
 405 410 415  
 Leu Val Met Pro  
 420

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met Ala Ser Glu Lys Gly Pro Ser Asn Lys Asp Tyr Thr Leu Arg Arg  
 1 5 10 15  
 Arg Ile Glu Pro Trp Glu Phe Glu Val Phe Phe Asp Pro Gln Glu Leu  
 20 25 30  
 Arg Lys Glu Ala Cys Leu Leu Tyr Glu Ile Lys Trp Gly Ala Ser Ser  
 35 40 45  
 Lys Thr Trp Arg Ser Ser Gly Lys Asn Thr Thr Asn His Val Glu Val  
 50 55 60  
 Asn Phe Leu Glu Lys Leu Thr Arg Lys Glu Ala Cys Leu Leu Tyr Glu  
 65 70 75 80  
 Ile Lys Trp Gly Ala Ser Ser Lys Thr Trp Arg Ser Ser Gly Lys Asn  
 85 90 95  
 Thr Thr Asn His Val Glu Val Asn Phe Leu Glu Lys Leu Thr Ser Glu  
 100 105 110  
 Gly Arg Leu Gly Pro Ser Thr Cys Cys Ser Ile Thr Trp Phe Leu Ser  
 115 120 125  
 Trp Ser Pro Cys Trp Glu Cys Ser Met Ala Ile Arg Glu Phe Leu Ser  
 130 135 140  
 Gln His Pro Gly Val Thr Leu Ile Ile Phe Val Ala Arg Leu Phe Gln  
 145 150 155 160  
 His Met Asp Arg Arg Asn Arg Gln Gly Leu Lys Asp Leu Val Thr Ser  
 165 170 175



Gly Val Thr Val Arg Val Met Ser Val Ser Glu Tyr Cys Tyr Cys Trp  
 180 185 190  
 Glu Asn Phe Val Asn Tyr Pro Pro Gly Lys Ala Ala Gln Trp Pro Arg  
 195 200 205  
 Tyr Pro Pro Arg Trp Met Leu Met Tyr Ala Leu Glu Leu Tyr Cys Ile  
 210 215 220  
 Ile Leu Gly Leu Pro Pro Cys Leu Lys Ile Ser Arg Arg His Gln Lys  
 225 230 235 240  
 Gln Leu Thr Phe Phe Ser Leu Thr Pro Gln Tyr Cys His Tyr Lys Met  
 245 250 255  
 Ile Pro Pro Tyr Ile Leu Leu Ala Thr Gly Leu Leu Gln Pro Ser Val  
 260 265 270  
 Pro Trp Arg  
 275

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GGATCTGACG GTTCACTAAA CCAGCTCTGC TTATATAGAC CTCCCACCGT ACACGCCTAC	60
CGCCCATTTG CGTCAATGGG GCGGAGTTGT TACGACATTT TGGAAAGTCC CGTTGATTTT	120
GGTGCCAAAA CAAACTCCAT TGACGTCAAT GGGGTGGAGA CTTGGAAATC CCCGTGAGTC	180
AAACCGCTAT CCACGCCCAT TGATGTACTG CCAAACCGC ATCACCATGG TAATAGCGAT	240
GACTAATACG TAGATGTACT GCCAAGTAGG AAAGTCCCAT AAGGTCATGT ACTGGGCATA	300
ATGCCAGGCG GGCCATTTAC CGTCATTGAC GTCAATAGGG GGCCTACTTG GCATATGATA	360
CACTTGATGT ACTGCCAAGT GGGCAGTTTA CCGTAAATAC TCCACCCATT GACGTCAATG	420
GAAAGTCCCT ATTGGCGTTA CTATGGGAAC ATACGTCATT ATTGACGTCA ATGGGCGGGG	480
GTCGTTGGGC GGTCAGCCAG GCGGGCCATT TACCGTAAGT TATGTAACGC GGAAGTCCAT	540
ATATGGGCTA TGAAGTAATG ACCCGTAAT TGATTACTAT TAATAACTA	589

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GATCCAAATC ACCCACTGCA ACTCCTCCCC CTGCG

35

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GATCCATCCA ATTGGGCAAT CAGGAG

26

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GATCCGGTCT CCAATTGG

18

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GATCCTCGGG AAAGGGAAAC CGAAACTGAA GCCG

34